

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 10:58:36 ; Search time 2197 Seconds
(without alignments)
9864.141 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcgcc.....atcaggaaagtggaatcgaaa 500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_in.*

18: em_mu.*

19: em_or.*

20: em_om.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_ro.*

26: em_sts.*

27: em_un.*

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JOURNAL Patent: WO 0240679-A 7 23-MAY-2002;
CRAFTON COREY M (US); RAYAPATI P JOHN (US)
FEATURES
source
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Location/Qualifiers
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"

ORIGIN

Query Match 100.0%; Score 500; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.8e-141; Indels 0; Gaps 0;
Matches 500; Conservative 0; Mismatches 0;
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Db 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACCACCGGTTTCGGCAACAATGACGGGAGAGA 60
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Db 61 GCCACACCATTCGATTCGGCTCCGATTAAGCCAGCGGCCCATATTTGCGAGGAGGATT 120
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Db 121 CGCCTGCGGTTTGGCGACATTCGGATCCCGGAAACCGAGCTCTGCAATGACCTGCGCGCG 180
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Db 181 AGGAAGCGAGGTGGGTGGCGAGGTTTGTAGTCGGGTTTAAAGCGTTGCCAGCGAGTGGT 240
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Qy 361 ACACCTGGTCTGACCAATTTTCGGACATAATCGGGCATAATTAAGGTGTAACAAGGA 420
Db 361 ACACCTGGTCTGACCAATTTTCGGACATAATCGGGCATAATTAAGGTGTAACAAGGA 420
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Db 421 ATCCGGGACAGCTCTGCTGATTTTCTGAGCTCTTGTGGGTTGTCCGGTTAGGGAA 480
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Db 481 ATCAGGAAGTGGATCGAAA 500

RESULT 2

AX127153/c
LOCUS AX127153 309400 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 7069 from Patent EP1108790.
ACCESSION AX127153 AX114121
VERSION AX127153.1 GI:14041141

SOURCE

Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE

1
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 7069 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)

FEATURES

source
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/note="Seq 1 to long (3.309.400) split in 11, seq 7069"

3.000.001 3.309.400 309.400"

ORIGIN

Query Match 98.1%; Score 490.4; DB 6; Length 309400;
Best Local Similarity 98.8%; Pred. No. 3e-137;
Matches 494; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 181 AGGAAGCGAGGTGGGTGGCGAGGTTTGTAGTCGGGTTTAAAGCGTTGCCAGCGAGTGGT 240
Db 113710 AGGAAGCGAGGTGGGTGGCGAGGTTTGTAGTCGGGTTTAAAGCGTTGCCAGCGAGTGGT 113651
Qy 241 AGCAAGACGCTAGTCTGGGAGCGAACCATTATTTAGTCACTTGGCAGAGCATGCACA 300
Db 113650 AGCAAGACGCTAGTCTGGGAGCGAACCATTATTTAGTCACTTGGCAGAGCATGCACA 113591
Qy 301 ATCTGCGAGGCGATAGATTGTTTGTCTCGATTTACAATGTGATTTTCAACAAAATA 360
Db 113590 ATCTGCGAGGCGATAGATTGTTTGTCTCGATTTACAATGTGATTTTCAACAAAATA 113531
Qy 361 ACACCTGGTCTGACCAATTTTCGGACATAATCGGGCATAATTAAGGTGTAACAAGGA 420
Db 113530 ACACCTGGTCTGACCAATTTTCGGACATAATCGGGCATAATTAAGGTGTAACAAGGA 113471
Qy 421 ATCCGGGACAGCTCTGCTGATTTTCTGAGCTCTTGTGGGTTGTCCGGTTAGGGAA 480
Db 113470 ATCCGGGACAGCTCTGCTGATTTTCTGAGCTCTTGTGGGTTGTCCGGTTAGGGAA 113411
Qy 481 ATCAGGAAGTGGATCGAAA 500
Db 113410 ATCAGGAAGTGGATCGAAA 113391

RESULT 3

AP005283/c
LOCUS AP005283 325651 bp DNA linear BCT 08-AUG-2002
DEFINITION Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section 10/10.

ACCESSION

AP005283 BA000036

VERSION

AP005283.1 GI:21325571

KEYWORDS

SOURCE

ORGANISM

Corynebacterium glutamicum ATCC 13032

Corynebacterium glutamicum ATCC 13032

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE

1

AUTHORS

Nakagawa,S.

TITLE

Complete genomic sequence of Corynebacterium glutamicum ATCC 13032

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 325651)

AUTHORS

Nakagawa,S.

TITLE

Direct Submission

JOURNAL

Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hako Kogyo Co. Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida, Tokyo 194-8533, Japan (E-mail:snakagawa@exanagen.com, Tel:81-44-829-3031, Fax:81-44-813-1851)

COMMENT

This sequence is conducted by collaboration of Kyowa Hako Kogyo Co. Ltd. And Kitasato University.

FEATURES

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VYKALKVSETRPGDFWISGVGGLHIAVQAAAMGRVIAVDIADDDKLEARKHGA
FTVNARNDEGEAVQKYNKINGAGHGLVTAHAAAFQALDARRAGTIVFNGLPPEF
PASVFNITVFKGLTIRGSLVGTQDLAELDFARGLIKPTVSEGLDEVNGLDRMEN
GKIDGRVAIRF"
/gene="Cg12808"
13402..13620
/note="Cg12808"
13402..13620
/codon_start=1

Query Match 98.1%; Score 490.4; DB 1; Length 325651;
Best Local Similarity 98.8%; Pred. No. 3e-137;
Matches 494; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACACCGGTTTCGGCAACAATGACGGCGAGAGA 60
Db 130141 AAAACAGCCAGGTTAGCGGCTGTAAACCCACACCGGTTTCGGCAACAATGACGGCGAGAGA 130082
Qy 61 GCCCACCACATTCGATTCGGCTCCGATTAAGCAGCGCCCATATTTCAGAGGAGGATT 120
Db 130081 GCCCACCACATTCGATTCGGCTCCGATTAAGCAGCGCCCATATTTCAGAGGAGGATT 130022
Qy 121 CGCCTGCGGTTTGGCGACATTCGGATCCCGGAACCGAGCTCTGCAATGACCTGCGCGCG 180
Db 130021 CGCCTGCGGTTTGGCGACATTCGGATCCCGGAACCGAGCTCTGCAATGACCTGCGCGCG 129962
Qy 181 AGGAAACGAGTGGGTGGCGAGTTTGTAGTCGGGTTTAAAGCGTTTCCAGCGAGTGGT 240
Db 129961 AGGAAACGAGTGGGTGGCGAGTTTGTAGTCGGGTTTAAAGCGTTTCCAGCGAGTGGT 129902
Qy 241 AGCAAGACGCTAGTCTGGGAGCGAACCACATATTGATGATCTCTGGCAGAGCATGCACA 300
Db 129901 AGCAAGACGCTAGTCTGGGAGCGAACCACATATTGATGATCTCTGGCAGAGCATGCACA 129842
Qy 301 ATCTCGAGGCGATAGATTGGTTTGTGCTGATTTACAAATGATGATTTTCAACAAAATA 360
Db 129841 ATCTCGAGGCGATAGATTGGTTTGTGCTGATTTACAAATGATGATTTTCAACAAAATA 129782
Qy 361 ACATTGGTCTGACCAATTTCCGACATATTCGGGACATATTCGGGATTAAGAGTGTAAACAAGGA 420
Db 129781 ACATTGGTCTGACCAATTTCCGACATATTCGGGACATATTCGGGATTAAGAGTGTAAACAAGGA 129722
Qy 421 ATCCGGGCAACAGCTCTGCTGATTTTCTGAGCTGCTTTGGGTTTCCGGTTAGGAGAA 480
Db 129721 ATCCGGGCAACAGCTCTGCTGATTTTCTGAGCTGCTTTGGGTTTCCGGTTAGGAGAA 129662
Qy 481 ATCAGGAAGTGGATCGAAA 500
Db 129661 ATCAGGAAGTGGATCGAAA 129642

RESULT 4
AX123295/c
LOCUS
DEFINITION Sequence 3211 from Patent EP1108790.
1776 bp DNA linear PAT 11-MAY-2001

AX123295
AX123295.1 GI:14040783
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 3211 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
FEATURES
source Location/Qualifiers
1..1776
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
ORIGIN
Query Match 52.8%; Score 264; DB 6; Length 1776;
Best Local Similarity 98.2%; Pred. No. 8e-69;
Matches 267; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACACCGGTTTCGGCAACAATGACGGCGAGAGA 60
Db 272 AAAACAGCCAGGTTAGCGGCTGTAAACCCACACCGGTTTCGGCAACAATGACGGCGAGAGA 213
Qy 61 GCCCACCACATTCGATTCGGCTCCGATTAAGCAGCGCCCATATTTCAGAGGAGGATT 120
Db 212 GCCCACCACATTCGATTCGGCTCCGATTAAGCAGCGCCCATATTTCAGAGGAGGATT 153
Qy 121 CGCCTGCGGTTTGGCGACATTCGGATCCCGGAACCGAGCTCTGCAATGACCTGCGCGCG 180
Db 152 CGCCTGCGGTTTGGCGACATTCGGATCCCGGAACCGAGCTCTGCAATGACCTGCGCGCG 93
Qy 181 AGGAAACGAGTGGGTGGCGAGTTTGTAGTCGGGTTTAAAGCGTTTCCAGCGAGTGGT 240
Db 92 AGGAAACGAGTGGGTGGCGAGTTTGTAGTCGGGTTTAAAGCGTTTCCAGCGAGTGGT 33
Qy 241 AGCAAGACGCTAGTCTGGGAGCGAACCACAT 272
Db 32 AGCAAGACGCTAGTCTGGGAGCGAACCACAT 1
RESULT 5
BD165412/c
LOCUS BD165412 1776 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel polynucleotide.
ACCESSION BD165412
VERSION BD165412.1 GI:27871224
KEYWORDS JP 2002191370-A/3211.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1776)
AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A.
TITLE Novel polynucleotide
JOURNAL Patent: JP 2002191370-A 3211 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
COMMENT OS Corynebacterium glutamicum
PN JP 2002191370-A/3211
PD 09-JUL-2002
PF 15-DEC-2000 JP 200405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
PI KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
PI OZAKI
PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC
C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12P7/40, C12P13/
PC 04, C12P13/08,

PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC
G01N33/566,
PC G01N33/569, G01N33/700//C12P21/08, (C12N1/21, C12R1/15),
PC (C12N1/21, C12R1/13), (C12N1/21, C12R1/01), (C12P13/08, C12R1/15),
PC C12N15/00,
PC C12N5/00, C12N15/00
CC Novel polynucleotide
FH Key Location/Qualifiers
FT source 1..1776
FT /organism='Corynebacterium glutamicum'.
FEATURES
source Location/Qualifiers
1..1776
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 52.8%; Score 264; DB 6; Length 1776;
Best Local Similarity 98.2%; Pred. No. 8e-69;
Matches 267; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AAAACAGCAGGTTAGCGCTGTAACCCACACGCTTTCGGCAACAATGACGCGAGAGA 60
DB 272 AAAACAGCAGGTTAGCGCTGTAACCCACACGCTTTCGGCAACAATGACGCGAGAGA 213
QY 61 GCCCACCACATTCGATTCCTCGATATAAGCCAGCGCCCATATTTTCAGGAGGATT 120
DB 212 GCCCACCACATTCGATTCCTCGATATAAGCCAGCGCCCATATTTTCAGGAGGATT 153
QY 121 CGCTCGGTTGGCGACATTCGATTCCTCGATATAAGCCAGCGCCCATATTTTCAGGAGGATT 180
DB 152 CGCTCGGTTGGCGACATTCGATTCCTCGATATAAGCCAGCGCCCATATTTTCAGGAGGATT 240
QY 181 AGGGAAGCAGGTTGGCGACATTCGATTCCTCGATATAAGCCAGCGCCCATATTTTCAGGAGGATT 272
DB 92 AGGGAAGCAGGTTGGCGACATTCGATTCCTCGATATAAGCCAGCGCCCATATTTTCAGGAGGATT 320
QY 241 AGCAAGAGCAGTGTCTGGGAGCGCAACCAT 272
DB 32 AGCAAGAGCAGTGTCTGGGAGCGCAACCAT 1

RESULT 6
AX763278 1084 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION
Sequence 95 from Patent WO03040291.
AX763278
VERSION
AX763278.1 GI:32257846
KEYWORDS
Corynebacterium glutamicum
SOURCE
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1
AUTHORS
Zelder, O., Pompejus, M., Schroeder, H., Kroeger, B., Kloppe, C. and
Haberhauer, G.
TITLE
Genes encoding for carbon metabolism and energy-producing proteins
Patent: WO 03040291-A 95 15-MAY-2003;
JOURNAL
BASF AKTIENGESSELLSCHAFT (DE)
FEATURES
source Location/Qualifiers
1..1084
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
101..1057
/note="unnamed protein product; RXA02694"
/codon_start=1
/translation="MKETVGNKIVLIGAGDVGVAYAYALINQGMADHIAIDIDEKLL
EGNVDLHNVWADSRTRVTKGTADCEADAMVVICAGAAKPGETRLQVLDKVKI
MKSIVGDMDSGDFGIFLVASNPVDILTAVYVWKFSGLEWNRVIGSGTGLDLSARFVYL
GELYEVPSPVHAYIIGHGDTELPVLSATAGVSLRMLDKDPELEGRLEKI
RDAVHIIIDAKGSTSYGIGMGLARITRAILQNDVAVPVSVALLHGEYGEDYIGTPA
VVRNGIRRVVELEITDHEMERFKHSANTLREIQKFF"

FEATURES

CDS

QY 401 ATAAAGGTGTAAACAAGGAATCCGGGCAACAAGCTTCTGCTGATTTCTGAGCTGCTTTG 460
DB 1 ATAAAGGTGTAAACAAGGAATCCGGGCAACAAGCTTCTGCTGATTTCTGAGCTGCTTTG 60
QY 461 TGGGTGTCGGTTAGGGAATCAGGAAGTGGATCGAAA 500
DB 61 TGGGTGTCGGTTAGGGAATCAGGAAGTGGATCGAAA 100

RESULT 8
AP005223/c
LOCUS
DEFINITION
Corynebacterium efficiens YS-314 DNA, complete genome, section
10/11.

ORIGIN

Query Match 22.4%; Score 112; DB 6; Length 1084;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 TAATCGGCGCATATTAAGGTGTAAACAAGGAATCCGGGCAACAAGCTTCTGCTGATTTTC 448
DB 1 TAATCGGCGCATATTAAGGTGTAAACAAGGAATCCGGGCAACAAGCTTCTGCTGATTTTC 60
QY 449 TGAGCTGCTTTGTCGGTTGTCGGTTAGGGAATCAGGAAGTGGATCGAAA 500
DB 61 TGAGCTGCTTTGTCGGTTGTCGGTTAGGGAATCAGGAAGTGGATCGAAA 112

RESULT 7

AX065003 1065 bp DNA linear PAT 24-JAN-2001
LOCUS
DEFINITION
Sequence 129 from Patent WO0100844.
AX065003
ACCESSION
AX065003.1 GI:12542715
KEYWORDS
Corynebacterium glutamicum
SOURCE
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1
AUTHORS
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G.
TITLE
Corynebacterium glutamicum genes encoding proteins involved in
carbon metabolism and energy production
Patent: WO 0100844-A 129 04-JAN-2001;
JOURNAL
BASF AKTIENGESSELLSCHAFT (DE)
FEATURES
source Location/Qualifiers
1..1065
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
101..1045
/note="unnamed protein product; RXA02694"
/codon_start=1
/translation="MKETVGNKIVLIGAGDVGVAYAYALINQGMADHIAIDIDEKLL
EGNVDLHNVWADSRTRVTKGTADCEADAMVVICAGAAKPGETRLQVLDKVKI
MKSIVGDMDSGDFGIFLVASNPVDILTAVYVWKFSGLEWNRVIGSGTGLDLSARFVYL
GELYEVPSPVHAYIIGHGDTELPVLSATAGVSLRMLDKDPELEGRLEKI
RDAVHIIIDAKGSTSYGIGMGLARITRAILQNDVAVPVSVALLHGEYGEDYIGTPA
VVRNGIRRVVELEITDHEMERFKHSANTLREIQKFF"

CDS

ORIGIN

Query Match 20.0%; Score 100; DB 6; Length 1065;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 401 ATAAAGGTGTAAACAAGGAATCCGGGCAACAAGCTTCTGCTGATTTCTGAGCTGCTTTG 460
DB 1 ATAAAGGTGTAAACAAGGAATCCGGGCAACAAGCTTCTGCTGATTTCTGAGCTGCTTTG 60
QY 461 TGGGTGTCGGTTAGGGAATCAGGAAGTGGATCGAAA 500
DB 61 TGGGTGTCGGTTAGGGAATCAGGAAGTGGATCGAAA 100

RESULT 8
AP005223/c
LOCUS
DEFINITION
Corynebacterium efficiens YS-314 DNA, complete genome, section
10/11.

ACCESSION	AP005223	BA000035	
VERSION	AP005223.1	GI:23494433	
KEYWORDS	Corynebacterium efficiens YS-314		
SOURCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.		
ORGANISM	Nishio, Y., Nakamura, Y., Kawarabayashi, Y., Usuda, Y., Kimura, E., Sugimoto, S., Matsui, K., Yamagishi, A., Kikuchi, H., Ikeo, K. and Gotohori, T.		
REFERENCE	Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens		
AUTHORS	Genome Res. 13 (7), 1572-1579 (2003)		
TITLE	2 (bases 1 to 302070)		
JOURNAL	Kawarabayashi, Y., Yamazaki, J., Hino, Y., Kikuchi, H. and Director-General of Biotechnology Center.		
MEDLINE	Submitted (17-MAY-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan		
PUBMED	(E-mail: bioemite.go.jp, Tel: 81-3-3481-1933, Fax: 81-3-3481-8424)		
REFERENCE	Kawarabayashi, Y. is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki, 305-8566 Japan		
AUTHORS	Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan		
TITLE	Icho, T. is at the Japan Biological Information Research Center, Koto-ku, Tokyo, 135-0064 Japan		
JOURNAL	Yamagishi, A. is at Tokyo University of Pharmacy and Life Science, Hachioji, Tokyo, 192-0392 Japan		
COMMENT	Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co., Inc., Kawasaki, Kanagawa, 210-8681 Japan		
FEATURES	The other authors are at the National Institute of Technology and Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.		
source	Location/Qualifiers		
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	/organism="Corynebacterium efficiens YS-314"		
	/mol_type="genomic DNA"		
	/strain="YS-314"		
	/db_xref="taxon:196164"		
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	/note="CE2590, similar to X89084-2 CAA61456.1 percent		
	identity: 85 in 397 aa"		
	/codon_start=1		
	/transl_table=11		
	/product="acetate kinase"		
	/protein_id="BAC19400.1"		
	/db_xref="GI:23494434"		
	/translation="MALALVINGSSSIKFQLVNPNANTDDPFVSLVQIGKMGKRIILKIRGEKVKEAPADHSGMSFDMTEHCGPQSOVDLIAVGRHVHGGILPSAPELLITELVEMIRDLPLAPLHPANIDGIEVARILLDPVHVAFTGPHSLPPAAALNADVAARVGIIRGFGHSHETVSSRVLDMPKPAEINITIFHIGNGASMAA VGGVAVDTSMGTPLAGLVMTGDTIDGFWPHLARNAMSIDEDINLNKKSQYKGLSGVDFRELHQMIEDGQDWSAYNIYIHLRRLYSYVALRGVLCIVFTAGVE NAHFVREDALAGLEMVGIKVDPERNKLPNQPRLLISTDDSTVKVFVPIPTNEALAIARYSAKFAE"		
	complement(1252..2766)		
	/note="CE2591, similar to AE006946-9 AAK4645.1 percent		
	identity: 45 in 495 aa"		
	/codon_start=1		
	/transl_table=11		
	/product="phosphate acetyltransferase"		
	/protein_id="BAC19401.1"		
	/db_xref="GI:23494435"		
	/translation="MRYRASNDAKLCEESQHLRPVPSGTHLVERITPDISSGLREERCMSPTTSALITVNRSPDFDLALADLEVLNLPVIRGDDFDMSKVLADLLADGPAIIVAGNAHFDQAALAGVPMGLVDRKSGSHVTLTAQKNVGAVVAATAFEBAKPKDKLKAVRNHNGALFVPMVAALFENMLKRAKEQAHVLPPEGDDRLTMAAHOLLEKDIICELTILGDPPEQIHSRATLGLHLEKADVINPLTDPKLDFAEQFABLRKSKGITLEQ		
	ARETMKDISYFGTMMVHNGDADGMVSGAANTTAHTIKPSQIITKTVPEASVVSIFLMVLGRWAFDCAVNPNTAEQGEIAVSAKTAQFGIDPRAVILSYSTGNSGTGPDVRAIDALAEARRIDPLKVDGPIQDAVPGVAKKMPDSDVAGHANVIFPDLEA		
	GNITYKTAQRTGHALAVGPILQGLNKFPVNDLSRGATVPDIVNTVAITAIQAGK"		
	3072..4511		
	/note="CE2592, similar to AE001908-11 AAF10073.1 percent		
	identity: 42 in 465 aa"		
	/codon_start=1		
	/transl_table=11		
	/product="putative ferredoxin/adrenodoxin reductase"		
	/protein_id="BAC19402.1"		
	/db_xref="GI:23494436"		
	/translation="MRFGCPPLPSGRDRQPMFKERKLSMSRPLRVAVVGAGPAGIYASDLMKSDHVDQIDLFERMAPFGLIRYGVAPDHPRIKGI1VKSLSHNVDKQQLRLGNI		
	EIGKDIITVDELREFYDAIIFSTGATGQDLRVKGAIDLEGSGAGFVFGVNDPFRGR		
	SWLSAEKVAIVGVGNVALDVARILAKTGBELKVEIPDNVYESLSQNKAREVHVFGR		
	RGPAAKFTPLELKELDSNIEVVNPDIDYDASEQARRDSKDLVCOITLQYA		
	IRDPKGPBKLFIFHFPESPVEILGDSKVGLKTERTRLDNGGVGVTGETTWDVQA		
	VYRAGVRSDAVRDVPDFDERRAIPNDGGRVIDPSTGSPVTSYATGWIRKGPILGIG		
	NTKSDAKETTEMILLADYAGSLPAPANPETAIIELDDRRKIPYTTWDGWHLLDAER		
	EAGEREGREKKIVWNWDMVRFARPEYEI"		
	4719..5261		
	/note="CE2593"		
	/codon_start=1		
	/transl_table=11		
	/product="hypothetical protein"		
	/protein_id="BAC19403.1"		
	/db_xref="GI:23494437"		
	/translation="MAMTVESVSNLAELSSLESHVHLKLVLDIFVHEOKTPYAEIDD		
	TDAIPTTRHILVWERHEDHTELGKCARLVPTTVTVEVAATGATLEDDAEVSQLGRV		
	AVSQDSRGTSLSAIMEAENALRAYEQPGKGVVLTALQLEFYEFGFTTCGTQYDE		
	AGVAPMVLKASELVYAA"		
	complement(5283..6560)		
	/note="CE2594, similar to AX064627-1 CAC25553.1 percent		
	identity: 86 in 401 aa"		
	/codon_start=1		
	/transl_table=11		
	/product="putative phosphoribosylglycinamide		
	formyltransferase"		
	/protein_id="BAC19404.1"		
	/db_xref="GI:23494438"		
	/translation="MSGVFTVSGSHMEFGAQTESQLFIPEKIGTFLSNATKVMIL		
	GSGELGKEVTIAFQRLGVEVHVDYNDPAHQVAHFSYVIDMTDAARVELVTIKP		
	DFIPIEALATDELRIEQEGLATVPTATQLTMTNREGIRLSEELGLPTSGYE		
	FCSTFEFTAAARLGPVNVKPMSSGKGQSVPTSAEDLSAGVAMSGAVSNOR		
	VIVQFVEFDYETLLTRGIDPATGKPAFCPIGHRQODGDGYVSWQPMEMTAPA		
	LENARSVAARITNALGGRGVGVGVLDVSGDDVFSVSPRHDTGLTLATORSEEE		
	LHAKAVGLPVDVTLTSPGASAVIYGVSDSPGVSYAGLAALAVAEITDRLFGKPEAF		
	TKRRMGVASTEDTATARDRATLAAAATVHG"		
	6584..7768		
	/note="CE2595, similar to AX064083-1 CAC25282.1 percent		
	identity: 38 in 391 aa"		
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	/transl_table=11		
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	/protein_id="BAC19405.1"		
	/db_xref="GI:23494439"		
	/translation="MNALLHNDTRADREELKYNFHRNPELSAEFTTIRTELK		
	NMDIKLIDVTATGAVAIENGQSPVVALRGDIDALPVTQTDGLDYASEAHGVMAHG		
	HDFHITLLSAVDVFAENRDKWSTGLVAVQPAAETASGARAVUEADIASVLPKDVY		
	LGQHWASQGVISMPETAVMTWESIRVRVFGTGTGSGMPHLGVDPDIVLAHITRL		
	QTVVAREISPFDFGVTVTGAINAGTKANIIIPESAELVNTRAMSEIQQKIRTAIERI		
	VRSECAAGAPAEFTFYDRAFLTNDADARSVAEAFNAQAFGEYQVTPPTASED		
	FSVIPDALGVYVFWFVGVEDPENAPGNHSPFPFAPVIOPTLDRSLAEAFITAAASALV		
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	7827..8417		
	/note="CE2596"		
	/codon_start=1		
	/transl_table=11		
	/product="hypothetical protein"		
	/protein_id="BAC19406.1"		
	/db_xref="GI:23494440"		
	/translation="MKTFRPLPLPKVPKVGSMRVATGAFAGTFAEPRWEKAGTLH		

TOIKTAMKSGRSGYKTIAPLOEMKLLPRVSAVSHEDAVVSELCTLVIAEDLQCGIQ
EFCVAPEHDCMKDARIIEYHAATSHLISAAALICARFDDNSPPPAIDTAMAFDAVF
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gene

Complement (8727..10016)

CDS

/gene="pura"

complement (8727..10016)

/BC_number="6.3.4.4"

/note="CE2597, similar to AL583918-8|CAC29788.1| percent

identity: 61 in 429 aa"

/codon_start=1

/transl_table=11

/product="adenylosuccinate synthetase"

/protein_id="BAC19407.1"

/db_xref="GI:2349441"

/translation="MAAIVVGAQWDEGKATDILGLVYVVKPNNAGHTVV
VGSEYELKLLPAGVLSEFATPILGNVVINLEALFEEDLGEARGADASRLRISANA
HLVAPYHQIMDRVQRFGLKRAIGTIGRGIGTYQKGRVGRVQDIFDESLRQKI
ESALDVKNQVLYNNRKAIVAEETVQVPLSYADRLRPMVIDATLELNKALDEGRHVL
MEGQATMLDDVHGTYFFVTSSNTAGACVSGVGPTITSLGIIKAYITRVGAGP
FTEFLDKWGEYLTQVGEVGNVTKRRCRQVSVIARYASRVNGFTDYFLTKLDVL
TGIGBIPICVAVEDVGRHDEMPMTQSDPHHAKPIFETMPANDEDITGCRTEELPQK
ADYVRLLEELSGARFSYIGVGPRDQITVLHDVMS"

CDS

10063..10989

/note="CE2598, similar to U23181-6|AAC48204.1| percent

identity: 20 in 247 aa"

/codon_start=1

/transl_table=11

/product="conserved hypothetical protein"

/protein_id="BAC19408.1"

/db_xref="GI:2349442"

/translation="MYAETLFTTPRAEFRRHNTKVVHMLRVILRCAPSPTDFPGA
PVAPEVHDLPEVTRDLMDDAFLVPHDPTSLDRIARQPDVHGLTQPAPQH
PROPLRIVIGSDLSLAVITRLRADNMVAEVYPTGESVAANKWGLPADPGAALR
LALTCVAKPVTIRDDAAVAVAGSATITDWEGETIGELIIVDDHVLVHREASPKTPRR
GIFGARLPMVAVPAGIAVMDTPAGTKKGLFRFRPTGTLPESLSLGRATQAGGP
SLRVTVDGMSVRKRAVERVTFYRHLRDLQVRP"

CDS

11033..11203

/note="CE2599"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="BAC19409.1"

/db_xref="GI:2349443"

/translation="WTPAGPAQLIIALVILVLFSGSKLPDVARSLGRSLRIFKSEIR
ELNRDSTTNQ"

CDS

complement (11200..12426)

/note="CE2600, similar to X17313-3|CAA35192.1| percent

identity: 74 in 359 aa"

/codon_start=1

/transl_table=11

Query Match 12.2%; Score 61.2; DB 1; Length 302070;

Best Local Similarity 65.2%; Pred. No. 1.3e-06;

Matches 90; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 2 AAACAGCCAGGTAGCGGTGTAACCCACCGGTTTCGGCAACAATGACGCGAGAGAG 61

Db 180389 ACACCGGAGGTGACCGCGGTGACCCACCAACCGCGGCGAGCGAGGTGACAGTG 180330

QY 62 CCCACACATTCGGATTCCGTCGATTAAGCCAGCGCCCATATTTGCGAGGAGATTC 121

Db 180329 CCCACAGGTGGCCATCTCCGACCGAGCGCGCGCCCATGCGGCGCGAGATCC 180270

QY 122 GCTCGGTTTGGCGACA 139

Db 180269 GCGCGGAGCGCGGCA 180252

RESULT 9

AC091879

LOCUS

DEFINITION Homo sapiens chromosome 5 clone CTD-3136G21, complete sequence.

AC091879

170712 bp DNA linear PRI 21-FEB-2002

Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint

ACCESSION

AC091879

VERSION AC091879.2 GI:18854959

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 170712)

AUTHORS

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE

Direct Submission

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 170712)

AUTHORS

DOE Joint Genome Institute.

TITLE

Direct Submission

JOURNAL

Unpublished

REFERENCE

3 (bases 1 to 170712)

AUTHORS

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE

Direct Submission

JOURNAL

Unpublished

COMMENT

On Feb 21, 2002 this sequence version replaced gi:14333815.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.1.

FEATURES

source

1..170712

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTD-3136G21"

ORIGIN

Query Match

Best Local Similarity 8.2%; Score 40.8; DB 9; Length 170712;

Matches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 280 CATCTGGCAGCATGCACAAATCTGCAGGCGATAGATTGTTTTCGATTACAAAT 339

Db 163012 CTTCTTAGCAAAATCTTACATAAATCAGAGAGATTGTATTCTATTCTTCAAG 163071

QY 340 GTGATTTTTCACAAAATAACACTTGGTCGACCAATTTTCGACATATCGGGCAT 399

Db 163072 GTGCTTAAAGGAAAAAAGGACAATCTCAAATTTTGTATTTCGAGATAAGCTTCAT 163131

QY 400 AATTAAAGGTGTAACAAAGGAATCCGGGCAACAGCTCTTGCTGA 443

Db 163132 AATGAAGGAGNAACAAAGTCTTTCCAGACAAACAATGCTGA 163175

RESULT 10

AC093298/c

LOCUS

AC093298

DEFINITION Homo sapiens chromosome 5 clone RP11-543J14, complete sequence.

ACCESSION AC093298

VERSION AC093298.3 GI:22038509

KEYWORDS

HTG.

SOURCE

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 198687)

AUTHORS

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE

Direct Submission

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 198687)

AUTHORS

DOE Joint Genome Institute.

TITLE

Direct Submission

JOURNAL

Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 198687)
 DOE Joint Genome Institute.
 Direct Submission
 Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 4 (bases 1 to 198687)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Direct Submission
 Submitted (01-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Aug 1, 2002 this sequence version replaced gi:19224834.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.7% of Sequence;
 Estimated Total Number of Errors is 0.4.

FEATURES
 source
 1. 198687
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="RP11-543L14"

ORIGIN
 Query Match 8.2%; Score 40.8; DB 9; Length 198687;
 Best Local Similarity 53.0%; Pred. No. 2;
 Matches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
 280 CATCTGCGCAGCATGCACAATCTGCGAGGCGATAGTTGGTTTGTGCGATTACAAT 339
 Db 196988 CTTCCTAGCAGAAATCTTACAATAATCAGAAGAGATTGTATCTATTCTTCAAG 196929
 340 GTGATTTTTCACAAAATAACACTTGGTCTGACCAATTTTCGGACATAATCGGCAT 399
 Db 196928 GTGCTTAAAGGAAAAAAGACAACTCTCAATTTTGTATTTTGCAGATAAGCTTCAT 196869
 400 AATTAAAGTGTTACAAAGGAATCGGCGCACAAAGCTCTTGTGTA 443
 Db 196868 AANTGAAGGAGAAACAAGTCTTCCGACACAAACAATGCTGA 196825

RESULT 11
 AC092837/c
 LOCUS AC092837 147820 bp DNA linear PRI 09-JAN-2002
 DEFINITION Homo sapiens BAC clone RP11-137J9 from 2, complete sequence.
 ACCESSION AC092837
 VERSION AC092837.5 GI:18098562
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 147820)
 Sulston, J.E. and Waterston, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1037-1108 (1998)
 99063792
 9847074
 PUBMED
 2 (bases 1 to 147820)
 Holmes, A., Boyer, E. and Meyer, R.
 The sequence of Homo sapiens BAC clone RP11-137J9
 Unpublished (2001)
 3 (bases 1 to 147820)
 Waterston, R.H.
 Direct Submission
 Submitted (30-JUL-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 147820)
 Waterston, R.

TITLE
JOURNAL

COMMENT

Direct Submission
 Submitted (09-JAN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jan 9, 2002 this sequence version replaced gi:15341615.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics

 Center project name: H_NH0137J09

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
 donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
 Tareno, M., Catanese, J.J. and de Jong, P.J. (1998). An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
 and coworkers at the Roswell Park Cancer Institute
 (http://bacpac.med.buffalo.edu)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-432012, 2000 bp overlap.
 Actual start of this clone is at base position 1 of RP11-137J9.

Polymorphisms have been identified between AC092837 and AC023468.

There is a transposon in the vector sequence.

FEATURES
source

1. 147820
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-137J9"
 /clone_lib="RP11-11"
 257. 651
 /rpt_family="CR1"
 868. 996
 /rpt_family="MIR"
 1308. 1608
 /rpt_family="Alu"
 2240. 2595
 /rpt_family="CR1"
 3976. 3998
 /rpt_family="AT-rich"
 3990. 4040
 /rpt_family="L1"
 4041. 4626
 /rpt_family="L1"
 4627. 5225
 /rpt_family="L1"

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repeat_region 5824..6117
/rpt_family="Alu"
repeat_region 7524..7566
/rpt_family="L2"
repeat_region 8276..8300
/rpt_family="(TG)n"
repeat_region 8628..8664
/rpt_family="A-rich"
repeat_region 9004..9049
/rpt_family="L2"
repeat_region 10005..10114
/rpt_family="MER1_type"
repeat_region 10943..11298
/rpt_family="MaLR"
repeat_region 11417..11554
/rpt_family="MIR"
repeat_region 11555..11903
/rpt_family="L1"
repeat_region 11952..11991
/rpt_family="MER1_type"
repeat_region 12012..12349
/rpt_family="MaLR"
repeat_region 12474..13249
/rpt_family="L1"
repeat_region 13068..13091
/rpt_family="(CAA)n"
repeat_region 13793..13954
/rpt_family="L1"
repeat_region 14264..14402
/rpt_family="Alu"
repeat_region 14412..14433
/rpt_family="AT-rich"
repeat_region 14546..14791
/rpt_family="L1"
repeat_region 15372..15581
/rpt_family="MIR"
repeat_region 15738..16030
/rpt_family="Alu"
repeat_region 16159..16242
/rpt_family="L2"
repeat_region 16651..16767
/rpt_family="MIR"
repeat_region 16769..17443
/rpt_family="L2"
repeat_region 17830..17871
/rpt_family="(CAA)n"
repeat_region 18615..18926
/rpt_family="L1"
misc_feature 18623..19078
/note="match to EST AI038529 (NID:G3277723) ox38e04.s1"
misc_feature 19691..20474
/note="match to EST BI917395 (NID:gl6181350)"
repeat_region 20713..21012
/rpt_family="Alu"
repeat_region 21198..21237
/rpt_family="(CA)n"
repeat_region 21298..22455
/rpt_family="L1"
repeat_region 22125..22152
/rpt_family="(TTG)n"
repeat_region 22591..22692
/rpt_family="MIR"
repeat_region 22693..23088
/rpt_family="MaLR"
repeat_region 22834..22886
/rpt_family="(TC)n"
repeat_region 23089..23233
/rpt_family="MIR"
repeat_region 23759..23822
/rpt_family="L2"
repeat_region 23823..24200
/rpt_family="MaLR"
repeat_region 24201..24435

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/rpt_family="L2"
24449..24561
/rpt_family="MaLR"
24562..24871
/rpt_family="MaLR"
24872..25036
/rpt_family="Alu"
25037..25145
/rpt_family="MaLR"
25146..25580
/rpt_family="MaLR"
25585..25931
/rpt_family="L2"
26016..26093
/rpt_family="L2"
28102..28644
/rpt_family="CR1"
28645..28934
/rpt_family="Alu"
28935..29001
/rpt_family="CR1"
29018..29235
/rpt_family="L2"
29348..29704
/rpt_family="L2"
29930..30296
/rpt_family="MaLR"

Query Match      8.0%; Score 40.2; DB 9; Length 147820;
Best Local Similarity 56.4%; Pred. No. 2.8;
Matches 75; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 323 TTGTCTCGATTTCACATGTGATTTTCAACAAAATAACACTTGTGCTGACCACATTTT 382
Db 142890 TATTTAGATPAATAATACATTTATTAATAATATATACACTTGTTCARATATCTT 142831

QY 383 CGACATATCGGGCATATTAAGGTGPAACAAAGGAATCCGGGCACAAAGCTCTTGCTG 442
Db 142830 GGGAAAGGAATGGGCATTCCTATATATGAACAAATCAGCTGAGTTAGTAATTGTTG 142771

QY 443 ATTTTCTGAGCTG 455
Db 142770 ATGCTGAGCGATG 142758

RESULT 12
AC004193
LOCUS Homo sapiens clone UMG:Y23c142 from 6p21, complete sequence.
DEFINITION AC004193
ACCESSION AC004193.1 GI:3980471
VERSION HTG
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 38194)
AUTHORS Janer, M., Guillaudoux, T., Vu, Q., Kutayavin, T., Harter, H. and
Geraghty, D.E.
TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 38194)
AUTHORS Geraghty, D.E. and Olson, M.V.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 38194)
AUTHORS Geraghty, D.E. and Olson, M.V.
TITLE Direct Submission

```

JOURNAL

Submitted (08-DEC-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

REMARK

University of Washington Human Genome Center
Box 352145 Seattle, WA 98195

COMMENT

Contact: Daniel E. Geraghty (geraghty@fhcr.org)
On Dec 8, 1998 this sequence version replaced gi:2905867.

Overlapping Sequences:

5' : UWGC:Y23C022 (Genbank Accession: AC004194)
3' : UWGC:Y23X010 (Genbank Accession: AC004172)

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part

of this entry's ASN.1 file.

Double stranded (DS) coverage: 90.7%

DS or two chemistry coverage: 100.0%

Single stranded regions: 0

Sequence Validation:

This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below.

Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

Map	Seq	HindIII		NsiI	
		Map	Seq	Map	Seq
3121.81	3124.00	2611.88	2559.00	1668.32	1694.00
6992.92	6962.00	2803.45	2806.00	2697.65	2688.00
2418.71	2395.00	5412.37	5370.00	5391.17	5365.00
1445.83	1463.00	7334.90	7251.00	1767.38	1763.00
4617.62	4628.00	513.70	507.00	1664.00	1668.00
11708.00	11842.00	1572.62	1604.00	2239.00	2203.00
		8080.50	7991.00	4106.00	4123.00
		689.00	682.00	5345.00	5423.00
		6102.00	5914.00	5345.00	5211.00
				1522.00	1537.00

FEATURES

source

Location/Qualifiers

1. 38194
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21"
/clone="CGM1:AL90C8"
/sub_clone="UWGC:Y23c142"
/cell_line="CGM1"
/clone_lib="Wash U YAC Library"
complement(322..612)
/rpt_family="Alu"
complement(4079..4376)
/rpt_family="Alu"
complement(4672..5947)
/rpt_family="Li"

repeat_region

repeat_region

repeat_region

repeat_region complement(6045..6157)
/rpt_family="Alu"
repeat_region complement(6453..6760)
/rpt_family="Alu"
repeat_region complement(7699..7796)
/rpt_family="Li"
repeat_region complement(8600..8736)
/rpt_family="Alu"
repeat_region complement(16938..17060)
/rpt_family="MLT1"
repeat_region 17202..17458
/rpt_family="LTR10"
repeat_region 18575..18862
/rpt_family="Alu"
repeat_region 19242..19518
/rpt_family="Alu"
repeat_region complement(22650..22763)
/rpt_family="Alu"
repeat_region complement(23124..23374)
/rpt_family="Alu"
repeat_region 23637..23904
/rpt_family="Alu"
repeat_region 23942..24393
/rpt_family="MLT2B2"
repeat_region complement(25520..25994)
/rpt_family="Li"
repeat_region complement(26071..26359)
/rpt_family="Alu"
repeat_region complement(26565..26672)
/rpt_family="Li"
repeat_region complement(28309..28449)
/rpt_family="MER20"
repeat_region 29016..29140
/rpt_family="Alu"
repeat_region 30585..30812
/rpt_family="MER30"
repeat_region 31405..31685
/rpt_family="Alu"
repeat_region complement(37038..37232)
/rpt_family="Alu"
repeat_region 38017..38191
/rpt_family="Alu"

ORIGIN

Query Match 8.0%; Score 40; DB 9; Length 38194;

Best Local Similarity 48.3%; Pred. No. 2.4;

Matches 112; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

Qy 47 ATGACGGGAGAGAGCCACACATTTGGATTTCGCTCCGATTAAGCCAGGCCCATAT 106
Db 13033 AGGCGGCGGACAGCCGCCCGGAGAGGGGCTGCCAAAGGCAACAGCCATAG 13092
Qy 107 TTGACAGGAGGATTTCGCTCGGTTTGGCGACATTCGGATCCCGGAACAGCTCTGCAA 166
Db 13093 GAGATGACAGGGTGCTCTGCTGGAGAACTCATCTCCCAACCCACCGATGCA 13152
Qy 167 TGACCTCGCGCCGAGGGAAGCGAGGTGGGTCGAGGTTTATGTCGGGTTTAAAGCGTTG 226
Db 13153 CAAGTAGAGGGCGAGGACAGCGAGGTTCGCGCGGATTCCGACCCCTCCCAACACC 13212
Qy 227 CCAGCGAGTGTGTAGCAAGACGCTAGTCTGGGAGGAGGAACCATATTGAG 278
Db 13213 GCCATGCGGCGGAGGAGAGACTACCGCGCGCAAGCAGAGAACGAGACGAG 13264

RESULT 13

EX001005/c

LOCUS

DEFINITION

Accession

Version

Keywords

Human DNA sequence from clone DAQB-346J13 on chromosome 6, complete sequence.
BX001005
BX001005
BX001005.6
GI:31335475
HTG.

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 50174)

TITLE Wood, J. Submission

JOURNAL Direct Submission

COMMENT Submitted (30-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 2, 2003 this sequence version replaced gi:30519606.

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6/MHC>
DAQB-346J13 is from a DNA-arts QBL human bac library VECTOR: pBelOBAC11.

FEATURES
source
1..50174
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="DAQB-346J13"
/clone_lib="DNA-arts-BAC.1-QBL.1"

ORIGIN
Query Match 7.7%; Score 38.4; DB 9; Length 50174;
Best Local Similarity 47.8%; Pred. No. 7.9;
Matches 111; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
QY 47 ATGACGGCAGAGAGCCACCATTCGCTTCGATTCGCTCGGATTAAGCCAGCCCATAT 106
Db 38224 AGCCCGCGGACAGCCACCCCGCGAGAGGGCTGCCAAAGGCAACAGCCATAG 38165
QY 107 TTGACGGAGGATTCGCTCGGTTGGCGACATTCGATTCGCCGGAACACGCTCTGCAA 166
Db 38164 GAGATGAGCAGGGGTGCTGCTGCTCGGAGAACTCATCTCCCAACCCACCGAGCCCA 38105
QY 167 TGACCTGCGCGCGAGGAGAGGAGTGGTGGCAGGTTTGTAGTCGGGTTTAAAGCGTTG 226
Db 38104 CAAGGTAGAGGCGAGACAGCGAGTTCGCCGATTCGCACTCCCTGCTCCAAACACC 38045
QY 227 CCAGGCGAGTGTGAGCAAGACGCTAGTCTGGGGAGCAAAACCATATTGAG 278
Db 38044 GCCATGGCGGGGAGGAGAGACTACCGCGCGCAAGCGNACGACGAG 37993

RESULT 14
AL645929/c
LOCUS
DEFINITION Human DNA sequence from clone Xxbac-1216 on chromosome 6, complete sequence.
AL645929
VERSION AL645929.4 GI:23093050
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 80662)
Griffiths, C.
Direct Submission
Submitted (12-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Sep 17, 2002 this sequence version replaced gi:18072572.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6/MHC>
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

FEATURES
Location/Qualifiers
1..80662
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="Xxbac-1216"
/clone_lib="CHORI-501"

ORIGIN
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Best Local Similarity 47.8%; Pred. No. 8.7;
Matches 111; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
QY 47 ATGACGGCAGAGAGCCACCATTCGCTTCGATTCGCTCGGATTAAGCCAGCCCATAT 106
Db 25805 AGCCCGCGGACAGCCACCCCGCGAGAGGGCTGCCAAAGGCAACAGCCATAG 25746
QY 107 TTGACGGAGGAGTTCGCTCGGTTGGCGACATTCGATTCGCCGGAACACGCTCTGCAA 166
Db 25745 GAGATGAGCAGGGGTGCTGCTGCTCGGAGAACTCATCTCCCAACCCACCGAGCCCA 25686
QY 167 TGACCTGCGCGCGAGGAGAGGAGTGGTGGCAGGTTTGTAGTCGGGTTTAAAGCGTTG 226

Db 25685 CAAGGTAGAGGGCGAGGACAGGAGGTGCGCGGATTCCGACCCCTCCCAACCACC 25626
 QY 227 CCAGGCGAGTGGTGAAGCAAGCGCTAGTCTGGGGAGCGAACCACATATTGAG 278
 Db 25625 GCCCATGGCGGGGAGGAGACTACCGACCGAAGCGGAAACGCAAGACGAG 25574

RESULT 15

AB023057 81561 bp DNA linear PRI 20-NOV-1999
 LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
 clone:779F20, complete sequence.
 ACCESSION AB023057
 VERSION AB023057.1 GI:5672626
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)
 AUTHORS Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
 Kikawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
 Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
 Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
 Bahram,S. and Inoko,H.

TITLE Molecular dynamics of MHC genesis unraveled by sequence analysis of
 the 1.796.938-bp HLA class I region

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

MEDLINE 20027539

PUBMED 10557312

REFERENCE 2 (bases 1 to 81561)

AUTHORS Shiina,T. and Takishima,N.

TITLE Direct Submission

JOURNAL Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of
 Medicine, Department of Molecular Life Science 2; Bohseidai,
 Isehara, Kanagawa 259-1193, Japan
 (E-mail:tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
 Fax:81-463-94-8884)

FEATURES

source
 1..81561
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.3"
 /clone="779F20"

ORIGIN

Query Match 7.7%; Score 38.4; DB 9; Length 81561;
 Best Local Similarity 47.8%; Pred. No. 8.8;
 Matches 111; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
 QY 47 ATGACGGCGAGAGACCCACCATTCGATTCGCTCGGATAAGCCAGCGCCCATAT 106
 Db 52642 AGGCGCGGGGACAGCCGCCACCGCGGAGAGGGGCTGCCAAAAGGCAACGACCATAG 52701
 QY 107 TTGACGGAGGATTTCGCTCGGTTTGGCGACATTCGGATCCCGGAAACAGCTCTGCAA 166
 Db 52702 GAGATGAGCAGGGGTGCTGCTGCTCGGAGACTCATCTCCCAACCCACCGACGCCA 52761
 QY 167 TGACCTGCGCGCGGAGGAGAGCGAGTGGGTGGCAGGTTTATGTCGGGTTTAAGCGTTG 226
 Db 52762 CAAGGTAGAGGGCGGAGACAGCGAGGTGCGGCCGATTTCGCGACCCCTGCCCTCAACACC 52821
 QY 227 CCAGGCGAGTGGTGAAGACGCTAGTCTGGGGAGCGAAACCATATTGAG 278
 Db 52822 GCCCATGGCGGGGAGAGAGATACCGCCCGCAACAGAACCGACAGAG 52873

Search completed: August 4, 2004, 12:43:55
 Job time : 2202 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 10:57:06 ; Search time 303 Seconds
(without alignments)
7010.228 Million cell updates/sec

Title: US-09-987-763-7
Perfect score: 500
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Maximum Match 100%
Listing first 45 summaries

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4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	500	100.0	500	6	ABQ73179	PA	Abq73179 C. glutam
2	490.4	98.1	309400	5	AAH68534	PA	Aah68534 C. glutam
3	264	52.8	1776	5	AAH68176	PI	Aah68176 C. glutam
4	264	52.8	1776	7	ACN01190	PI	Aco01190 C. glutam
5	112	22.4	1084	9	ADD13410	XX	Add13410 C. glutam
6	100	20.0	1065	4	AAF71424	XX	Aaf71424 Corynebact
7	36.4	7.3	1263	9	ADC90725	XX	Adc90725 E. faeciu
8	36.4	7.3	2000	7	ACC61930	XX	Acc61930 Gene sequ
9	36.2	7.2	1053	7	ACA42017	XX	Aca42017 Prokaryot
10	34.8	7.0	6210	2	AXX02986	XX	Aax02986 Human li-
11	33.2	6.6	4613	4	ABU11796	XX	Abu11796 Drosophil
12	32.8	6.6	32191	4	AAS30497	XX	Aae30497 DNA encod
13	32.8	6.6	32191	4	AAL06277	XX	Aal06277 Human rep
14	32.8	6.6	46107	4	AAK71730	XX	Aak71730 Human imm
15	32.6	6.5	257	6	ABN16341	XX	Abn16341 Human ORF
16	32.4	6.5	579	6	ABN62193	XX	Abn62193 Human can
17	32.4	6.5	1666	6	ABQ34526	XX	Abq34526 Oligonuc
18	32.4	6.5	1666	6	ABQ34527	XX	Abq34527 Oligonuc
19	32.2	6.4	3108	6	ABN59617	XX	Abn59617 Novel hum
20	32.2	6.4	3690	9	ADC37644	XX	Adc37644 Human nuc
21	32	6.4	577	4	AAI42479	XX	Aai42479 Probe fil
22	32	6.4	577	4	ABS36372	XX	Abs36372 Human liv
23	32	6.4	577	6	ABS10712	XX	Abs10712 Human gen

C	24	32	6.4	2000	7	ADA71938	Ada71938 Rice gene
C	25	31.8	6.4	1295	7	ACD93559	AcD93559 Human col
C	26	31.8	6.4	1308	7	ACA43692	Aca43692 Prokaryot
C	27	31.6	6.3	866	8	ADB07101	AdB07101 Allostoc
C	28	31.6	6.3	2625	3	AAc60048	Aac60048 Human sec
C	29	31.6	6.3	2625	7	ADA97959	Ada97959 Human sec
C	30	31.6	6.3	2625	7	ADA43865	Ada43865 Human sec
C	31	31.6	6.3	2625	9	ADC20114	Adc20114 Human sec
C	32	31.6	6.3	19403	4	ABU11856	Abu11856 Drosophil
C	33	31.6	6.3	57130	7	ABQ77243	Abq77243 Human MAR
C	34	31.6	6.3	110000	8	ADB12064_02	Continuation (3 of
C	35	31.4	6.3	636	7	ACF68771	AcF68771 Photorhab
C	36	31.4	6.3	848	2	AAZ17390	Aaz17390 Human gen
C	37	31.4	6.3	2512	7	ABZ35845	Abz35845 Human sec
C	38	31.4	6.3	3923	7	ABX08775	Abx08775 Angiogene
C	39	31.4	6.3	24526	6	ADA43979	Ada43979 Human tra
C	40	31.4	6.3	26565	6	ABS78924	Abs78924 E. coli C
C	41	31.4	6.3	110000	7	ACF67367_15	Continuation (16 o
C	42	31.4	6.3	249878	7	ACF65381	AcF65381 Photorhab
C	43	31.2	6.2	536	9	ADB68842	AdB68842 Minority
C	44	31.2	6.2	629	6	ABQ53668	Abq53668 Oligonuc
C	45	31.2	6.2	629	6	ABQ53669	Abq53669 Oligonuc

ALIGNMENTS

RESULT 1
ABQ73179
ID ABQ73179 standard; DNA; 500 BP.
XX
AC ABQ73179;
XX
DT 27-SEP-2002 (first entry)
XX
DE C. glutamicum transcriptional regulatory region ldh DNA SEQ ID NO:7.
XX
KW Corynebacterium glutamicum; gene expression;
KW amino acid biosynthesis; gene; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200240679-A2;
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-US043096.
XX
PR 15-NOV-2000; 2000US-0248219P.
XX
PA (RAYA/) RAYAPATI P J.
(CRAP/) CRAFTON C M.
XX
PI Rayapati PJ, Crafton CM;
XX
XX WPI; 2002-575217/61.
XX
PT Novel polynucleotides from Corynebacterium glutamicum useful for inducing
PT and regulating expression of genes, including those that are involved in
PT amino acid biosynthesis, in bacterial cells.
XX
XX Claim 20; Page 25; 112pp; English.
XX
CC The present invention describes Corynebacterium glutamicum
transcriptional regulatory region polynucleotide sequences (I). ABQ73173
to ABQ73194 represent the C. glutamicum transcriptional regulatory
regions pta, aceA, aceB, adh, aldB, poxB, ldh, amyE, malZ, bglX, gam,
glxX, hisD, pyrR, purD, hrcA, htpX, dnaK, etc, grpE, and narX,
respectively. (I) can be used for producing a vector. (I) can also be
used for producing a transformed Corynebacterium sp. host cell, which is
useful for producing a biosynthetic product. (I) is useful for producing
a Corynebacterium sp. host cell, which is useful for producing an amino
acid. (I) is useful for regulating and enhancing the production of a

CC variety of products in host cells, including amino acids such as lysine,
 CC purine nucleotides such as inosinic acid, and heterologous polypeptides
 XX
 SQ Sequence 500 BP; 127 A; 110 C; 145 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 500; DB 6; Length 500;
 Best Local Similarity 100.0%; Pred. No. 3.9e-155;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAACAGCCAGGTTAGCGGTGTAACCCACACCGTTTCGGCAACATGACGGGAGAGA 60
 Db 1 AAAACAGCCAGGTTAGCGGTGTAACCCACACCGTTTCGGCAACATGACGGGAGAGA 60
 Qy 61 GCCCACCACATTCGATTCGCTCCGATAAAGCCAGCGCCATATTTGACGGGAGGATT 120
 Db 61 GCCCACCACATTCGATTCGCTCCGATAAAGCCAGCGCCATATTTGACGGGAGGATT 120
 Qy 121 CGCCTGCGGTTTGGCGACATTCGATCCCGAAACCGACTCTGCAATGACCTGCGCGCG 180
 Db 121 CGCCTGCGGTTTGGCGACATTCGATCCCGAAACCGACTCTGCAATGACCTGCGCGCG 180
 Qy 181 AGGAAAGCGAGTGGTGGCAGGTTTGTAGTCGGGTTTAAAGTTCGAGCGAGTGGTG 240
 Db 181 AGGAAAGCGAGTGGTGGCAGGTTTGTAGTCGGGTTTAAAGTTCGAGCGAGTGGTG 240
 Qy 241 AGCAAAAGACGCTAGTCTGGGAGCGAAACCATATTTGATCATCTTGGCAGAGCATGCACA 300
 Db 241 AGCAAAAGACGCTAGTCTGGGAGCGAAACCATATTTGATCATCTTGGCAGAGCATGCACA 300
 Qy 301 ATCTGCGAGGCGATAGATTGGTTTGTCTCGATTTACAAATGATTTTTCACAAAATA 360
 Db 301 ATCTGCGAGGCGATAGATTGGTTTGTCTCGATTTACAAATGATTTTTCACAAAATA 360
 Qy 361 ACACCTGGTCTGACACATTTTCGACATATTCGGACATAATCGGGCATAATTAAGGTGTAACAAAGGA 420
 Db 361 ACACCTGGTCTGACACATTTTCGACATATTCGGACATAATCGGGCATAATTAAGGTGTAACAAAGGA 420
 Qy 421 ATCCGGGCGACAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 480
 Db 421 ATCCGGGCGACAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 480
 Qy 481 ATCAGGAAGTGGGATCGAAA 500
 Db 481 ATCAGGAAGTGGGATCGAAA 500

RESULT 2
 AAH68534/c
 ID AAH68534 standard; DNA; 309400 BP.

XX AC AAH68534;

XX DT 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 7069.

XX Corynebacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-00127688.

XX 16-DEC-1999; 99JP-00377484.

XX 07-APR-2000; 2000JP-00159162.

XX 03-AUG-2000; 2000JP-00280988.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40.

XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.

PS The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium, measuring expression amount and analyzing
 CC the expression profile or expression pattern of a gene derived from
 CC Corynebacterium, and identifying a homologue of a gene derived from
 CC Corynebacterium. Corynebacterium bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the European Patent Office

XX SQ Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;

Query Match 98.1%; Score 490.4; DB 5; Length 309400;
 Best Local Similarity 98.8%; Pred. No. 1.6e-150;
 Matches 494; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AAAACAGCCAGGTTAGCGGTGTAACCCACACCGTTTCGGCAACATGACGGGAGAGA 60
 Db 113890 AAAACAGCCAGGTTAGCGCGGTAAACCCACACCGTTTCGGCAACATGACGGGAGAGA 113831
 Qy 61 GCCCACCACATTTGCGATTTCCGCTCCGATAAAGCCAGCGCCATATTTGACGGGAGGATT 120
 Db 113830 GCCCACCACATTTGCGATTTCCGCTCCGATAAAGCCAGCGCCATATTTGACGGGAGGATT 113771
 Qy 121 CGCCTGCGGTTTGGCGACATTCGATCCCGAAACCGACTCTGCAATGACCTGCGCGCG 180
 Db 113770 CGCCTGCGGTTTGGCGACATTCGATCCCGAAACCGACTCTGCAATGACCTGCGCGCG 113711
 Qy 181 AGGAAAGCGAGTGGTGGCAGGTTTGTAGTCGGGTTTAAAGTTCGAGCGAGTGGTG 240
 Db 113710 AGGAAAGCGAGTGGTGGCAGGTTTGTAGTCGGGTTTAAAGTTCGAGCGAGTGGTG 113651
 Qy 241 AGCAAAAGACGCTAGTCTGGGAGCGAAACCATATTTGATCATCTTGGCAGAGCATGCACA 300
 Db 113650 AGCAGAGACGCTAGTCTGGGAGCGAAACCATATTTGATCATCTTGGCAGAGCATGCACA 113591
 Qy 301 ATCTGCGAGGCGATAGATTGGTTTGTCTCGATTTACAAATGATTTTTCACAAAATA 360
 Db 113590 ATCTGCGAGGCGATAGATTGGTTTGTCTCGATTTACAAATGATTTTTCACAAAATA 113531
 Qy 361 ACACCTGGTCTGACACATTTTCGACATATTCGGACATAATCGGGCATAATTAAGGTGTAACAAAGGA 420
 Db 113530 ACACCTGGTCTGACACATTTTCGACATATTCGGACATAATTAAGGTGTAACAAAGGA 113471
 Qy 421 ATCCGGGCGACAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 480
 Db 113470 ATCCGGGCGACAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 113411
 Qy 481 ATCAGGAAGTGGGATCGAAA 500
 Db 113410 ATCAGGAAGTGGGATCGAAA 113391

RESULT 3
 AAH68176/c
 ID AAH68176 standard; DNA; 1776 BP.
 XX
 AC AAH68176;
 XX

ID ADD13410 standard; DNA; 1084 BP.
 XX
 AC ADD13410;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE C. glutamicum carbon metabolism associated DNA RXA02694.
 XX
 DE ds; gene; carbon metabolism; energy-rich molecule;
 XX oxidative phosphorylation; fine chemical; amino acid production;
 KW lysine production; nucleotide production; nucleoside production;
 KW lipid production; fatty acid production; diol production;
 KW carbohydrate production; aromatic compound production;
 KW vitamin production; co-factor production; enzyme production; food;
 KW animal feed; cosmetic; pharmaceutical.
 XX
 XX Corynebacterium glutamicum.
 XX
 XX Key Location/Qualifiers
 FT CDS 101..1057
 FT /*tag= a
 XX
 XX WO2003040291-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 31-OCT-2002; 2002WO-EP012135.
 XX
 XX 05-NOV-2001; 2001DE-01054270.
 XX
 XX (BADI) BASF AG.
 XX
 XX Zelder O, Pompejus M, Schroeder H, Kroeger B, Kloppegg C;
 PI Haberhauer G;
 PI
 XX
 XX WPI; 2003-505068/47.
 DR P-PSDB; ADD13411.
 XX
 XX New nucleic acid encoding variant forms of proteins involved in carbon
 PT compound metabolism, useful for production of fine chemicals,
 PT specifically lysine, in microorganisms.
 XX
 XX Claim 1; SEQ ID NO 95; 259pp; German.
 PS
 XX
 CC This invention describes novel polynucleotides and polypeptides
 CC associated with the metabolism of carbon compounds and generation of
 CC energy-rich molecules by oxidative phosphorylation in Corynebacterium
 CC glutamicum. The polynucleotides of the invention are isolated from a
 CC nucleic acid library of C. glutamicum then mutated at the specified
 CC positions, cloned and expressed by standard methods. Cells, especially
 CC Corynebacterium glutamicum, containing vectors that express the
 CC polynucleotides are used for production of fine chemicals, preferably
 CC amino acids and specifically lysine, but more generally nucleotides,
 CC nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, co-factors and enzymes. These are useful in the
 CC food, animal feed, cosmetics and pharmaceutical industries.
 CC polynucleotides, optionally as primers and probes, can also be used for
 CC identification and classification of C. glutamicum and related species,
 CC e.g. for diagnosis; for genomic mapping; functional or evolutionary
 CC studies gene manipulation, and modulation of metabolic activity. Cells
 CC that contain the products of the invention may produce fine chemicals in
 CC better yields, with higher productivity and/or more efficiently.
 XX
 XX Sequence 1084 BP; 270 A; 308 C; 285 G; 221 T; 0 U; 0 Other;
 SQ
 Query Match 22.4%; Score 112; DB 9; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 3.3e-26;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 389 TAATCGGCATTAATTAAGGCTGTAACAAGGAATCCGGGCAACGCTTGTGCTATTTC 448
 DB 1 TAATCGGCATTAATTAAGGCTGTAACAAGGAATCCGGGCAACGCTTGTGCTATTTC 60

QY 449 TGAGCTGCTTTGGGTTGTTCGGTTAGGGAATCAGGAAGTGGATCGAAA 500
 ID AAF71424 standard; DNA; 1065 BP.
 DB 61 TGAGCTGCTTTGGGTTGTTCGGTTAGGGAATCAGGAAGTGGATCGAAA 112
 RESULT 6
 AAF71424
 ID AAF71424 standard; DNA; 1065 BP.
 XX
 AC AAF71424;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:129.
 XX
 XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX
 XX Corynebacterium glutamicum.
 OS
 XX WO200100844-A2.
 XX
 XX 04-JAN-2001.
 XX
 XX 23-JUN-2000; 2000WO-IB000943.
 PF
 XX 25-JUN-1999; 99US-0141031P.
 PR 08-JUL-1999; 99DE-01031412.
 PR 08-JUL-1999; 99DE-01031413.
 PR 08-JUL-1999; 99DE-01031419.
 PR 08-JUL-1999; 99DE-01031420.
 PR 08-JUL-1999; 99DE-01031424.
 PR 08-JUL-1999; 99DE-01031428.
 PR 08-JUL-1999; 99DE-01031431.
 PR 08-JUL-1999; 99DE-01031433.
 PR 08-JUL-1999; 99DE-01031434.
 PR 08-JUL-1999; 99DE-01031510.
 PR 08-JUL-1999; 99DE-01031562.
 PR 08-JUL-1999; 99DE-01031634.
 PR 09-JUL-1999; 99DE-01032180.
 PR 09-JUL-1999; 99DE-01032227.
 PR 09-JUL-1999; 99DE-01032230.
 PR 09-JUL-1999; 99US-0143208P.
 PR 14-JUL-1999; 99DE-01032324.
 PR 14-JUL-1999; 99DE-01032973.
 PR 14-JUL-1999; 99DE-01033005.
 PR 27-AUG-1999; 99DE-01040765.
 PR 31-AUG-1999; 99US-0151572P.
 PR 03-SEP-1999; 99DE-01042076.
 PR 03-SEP-1999; 99DE-01042086.
 PR 03-SEP-1999; 99DE-01042087.
 PR 03-SEP-1999; 99DE-01042088.
 PR 03-SEP-1999; 99DE-01042095.
 PR 03-SEP-1999; 99DE-01042123.
 PR 03-SEP-1999; 99DE-01042125.
 XX
 XX (BADI) BASF AG.
 XX
 XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
 XX WPI; 2001-061975/07.
 DR P-PSDB; AAB79307.
 XX
 XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes.

XX
PS Claim 3; Page 332-333; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 1065 BP; 264 A; 304 C; 279 G; 218 T; 0 U; 0 Other;
Query Match 20.0%; Score 100; DB 4; Length 1065;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 401 ATTAAAGGTGTAAACAAAGGAATCCGGCACAGCTCTTCGATTTCTGAGCTGCTTTG 460
DB 1 ATTAAAGGTGTAAACAAAGGAATCCGGCACAGCTCTTCGATTTCTGAGCTGCTTTG 60
QY 461 TGGGTTGTCGCTTAGGGAATCAGGAAGTGGGATCGAAA 500
DB 61 TGGGTTGTCGCTTAGGGAATCAGGAAGTGGGATCGAAA 100
RESULT 7
ADC90725/c
ID ADC90725 standard; DNA; 1263 BP.
XX
AC ADC90725;
XX
XX
DT 01-JAN-2004 (first entry)
XX
DE E. faecium DNA sequence SEQ ID 352.
XX
KW ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX
OS Enterococcus faecium.
XX
PN US6583275-B1.
XX
PD 24-JUN-2003.
XX
PF 30-JUN-1998; 98US-00107532.
XX
PR 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-799836/75.
DR P-PSDB; ADC94379.
XX
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX

PS Example 1; SEQ ID NO 352; 243pp; English.
XX
CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids are useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC nucleic acid is useful for recombinant production of candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium nucleic acids.
XX
SQ Sequence 1263 BP; 338 A; 245 C; 244 G; 436 T; 0 U; 0 Other;
Query Match 7.3%; Score 36.4; DB 9; Length 1263;
Best Local Similarity 53.5%; Pred. No. 0.43;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 292 GCATGCACAAATTCGCGGGCATAGATTGTTTGTCTCGATTACATGTGATTTTCA 351
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QY 352 ACAAAATAACACTTGGTCTGACCACATTTTCGGACATAATCGGCATATAAAGGTGT 411
DB 233 CTAATCAAAACAAATAAGTAGTACCATAAAGAGGAGGAGCGTGAATTAATTCACAGCA 174
QY 412 AACAAAGGAATCCGGGCACAAG 433
DB 173 GATAAAGAACGGTGGCGCATAG 152
RESULT 8
ACC61930
ID ACC61930 standard; DNA; 2000 BP.
XX
AC ACC61930;
XX
DT 20-JUN-2003 (first entry)
XX
DE Gene sequence #SEQ ID 2642.
XX
KW Multiprotein complex; eukaryote; drug target; diagnosis; gene; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN EP1258494-A1.
XX
PD 20-NOV-2002.
XX
PF 20-DEC-2001; 2001EP-00130253.
XX
PR 15-MAY-2001; 2001EP-00111774.
XX
XX (CELL-) CELLZONE AG.
XX
XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
PI Marzioch M, Schultz JD, Superti-Furga GD;
XX
XX WPI; 2003-250078/25.
DR P-PSDB; ABR53888.
XX
XX New isolated protein complexes useful for diagnosing a disease or
PT disorder, or as a target for an active agent of a pharmaceutical,
PT preferably a drug target in the treatment or prevention of disease or
PT

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the targeted prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://wipo.int/pub/published/pct/sequences)

PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209457P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
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 PR 14-JUL-2000; 2000US-0218290P.
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 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
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 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.
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 PR 08-DEC-2000; 2000US-0251856P.
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 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2001US-0259497P.
 PR 05-JAN-2001; 2001US-0259578P.

(HUMA-) HUMAN GENOME SCI INC.

FI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-476223/51.

XX Novel isolated prostate gland related polypeptide useful for diagnosis
 PT and treatment of disorders of prostate such as prostatodystonia,
 PT prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia.

XX Claim 1; SEQ ID NO 355; 512pp; English.

XX The invention relates to novel isolated prostate gland related nucleic
 CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,

RESULT 13	
AA106277/c	
ID	AA106277 standard; DNA; 32191 BP.
XX	
XX	AA106277;
XX	
XX	
DT	21-NOV-2001 (first entry)
XX	
DE	Human reproductive system related antigen DNA SEQ ID NO: 8965.
XX	
KW	Human; reproductive system related antigen; reproductive system disorder;
KW	cancer; gene therapy; ds.
XX	
XX	
OS	Homo sapiens.
XX	
PN	WO200155320-A2.
XX	
PD	
XX	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US001339.
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PR	31-JAN-2000; 2000US-0179065P.
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PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.

Db 30706 TGAAGTCACCGCCCTCCTA 30687

Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 206 TTAGTCCGGGTTTAAAGCGTTGCCAGCGAGTGGTGGAGCAAGACGCTAGTCTGGGAGCG 265
Db 110 TCATTCCGGGTTTCAACCGGAGCCCGGACCTGGTGCAAAAGGACGTGCCAGGAGGC 169
QY 266 AAACCATATTGAGTCATCTTGGCAGAGCATGCAACAATTCTGCA 308
Db 170 CAAAGGTGCGGTGAGCCCTGCATAGCCCCCACTAGATGCA 212

Search completed: August 4, 2004, 12:06:56
Job time : 307 secs

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ID ABN16341 standard; cDNA; 257 BP.
XX
XX AC ABN16341;
XX
XX 24-JUN-2002 (first entry)
XX
XX DE Human ORFX polynucleotide sequence SEQ ID NO:1159.
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; Gene; ss.
XX
XX OS Homo sapiens.
XX
XX FN WO200192523-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 29-MAY-2001; 2001WO-US010836.
XX
XX FR 30-MAY-2000; 2000US-0206132P.
XX
XX PR 29-AUG-2000; 2000US-0228716P.
XX
XX PA (CURA-) CURAGEN CORP.
XX
XX FI Shimkets RA, Leach MD;
XX
XX DR WPI; 2002-106308/14.
XX
XX DR P-PSDB; ABP00589.
XX
XX PT Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.
XX
XX PS Disclosure; SEQ ID NO 1159; 1037pp; English.
XX
XX CC The present invention describes substantially purified human proteins
XX (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX in the specification). ABN15762 to ABN27252 encode the human ORFX
XX proteins given in ABP0010 to ABP11500. ORFX proteins are useful for
XX treating or preventing a pathology associated with an ORFX-associated
XX disorder in humans, and in the manufacture of a medicament for treating a
XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX sequences can be used in gene therapy. ORFX sequences can be used in the
XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
XX osteoarthritis, neurodegenerative disorders, disorders related to organ
XX transplantation, cardiovascular diseases, diabetes mellitus, systemic
XX lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
XX storage disease, various immune deficiencies and disorders, infectious
XX diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
XX arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
XX disease and autoimmune inflammatory eye disease. ORFX proteins are also
XX useful for treating burns, incisions, ulcers, for treating osteoporosis,
XX bone degenerative disorders, or periodontal disease, and for gut
XX protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues and conditions resulting from
XX systemic cytokine damage. N.B. The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 257 BP; 53 A; 65 C; 99 G; 40 T; 0 U; 0 Other;

Query Match 6.5%; Score 32.6; DB 6; Length 257;
Best Local Similarity 57.3%; Pred. NO. 3.5;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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4404.372 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 5: /cgn2_6/ptodata/2/ina/6C COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/6D COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	34.8	7.0	152331	3	US-09-128-155-16
C 3	33.4	6.7	468	4	US-09-252-991A-15459
C 4	33.4	6.7	1014	4	US-09-252-991A-15280
C 5	33.4	6.7	1842	4	US-09-252-991A-15508
C 6	32.4	6.5	831	4	US-09-489-039A-2499
C 7	31.2	6.2	732	4	US-09-134-000C-348
C 8	31	6.2	1825	4	US-09-976-594-673
C 9	31	6.2	2163	4	US-09-134-000C-2226
C 10	31	6.2	2640	4	US-08-684-932A-37
C 11	31	6.2	2655	4	US-09-016-434-1094
C 12	31	6.2	2655	4	US-09-023-655-916
C 13	30.6	6.1	392000	4	US-10-027-983-11
C 14	30.4	6.1	5722	4	US-09-566-921-54
C 15	30	6.0	426	3	US-09-441-346A-3
C 16	30	6.0	426	3	US-09-789-453A-3
C 17	30	6.0	455	4	US-09-621-976-10754
C 18	30	6.0	2847	4	US-09-484-970B-22
C 19	29.8	6.0	162	4	US-09-017-754A-6
C 20	29.8	6.0	255	4	US-09-516-667-85
C 21	29.6	5.9	921	4	US-09-489-039A-6123
C 22	29.6	5.9	17846	4	US-08-956-171E-109
C 23	29.4	5.9	7218	1	US-08-232-463-14
C 24	29.4	5.9	1830121	4	US-09-557-884-1
C 25	29.4	5.9	1830121	4	US-09-643-950A-1
C 26	29.2	5.8	1158	4	US-09-545-569A-9
C 27	29.2	5.8	1164	4	US-09-545-569A-1

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Sequence 1, Appli
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Sequence 11597, A

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33 29.2 5.8 3967 4 US-09-672-749-14
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35 29.2 5.8 193303 4 US-09-497-855A-37
36 29.2 5.8 193303 4 US-09-497-855A-44
37 29 5.8 500 3 US-09-141-000-2
38 29 5.8 3048 1 US-07-921-807B-1
39 29 5.8 3048 1 US-08-441-944A-1
40 29 5.8 40328 3 US-08-742-185-102
41 29 5.8 319608 4 US-09-539-333D-1
42 29 5.8 319608 4 US-09-679-409-1
43 29 5.8 4403765 3 US-09-103-840A-2
44 29 5.8 4411529 3 US-09-103-840A-1
45 28.8 5.8 534 4 US-09-252-991A-11597

ALIGNMENTS

RESULT 1

US-09-107-532A-352/c

; Sequence 352, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Denke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 352:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1263 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...1263

; CURRENT APPLICATION NUMBER: US/09/252,991A									
; CURRENT FILING DATE: 1999-02-18									
; PRIOR APPLICATION NUMBER: US 60/074,788									
; PRIOR FILING DATE: 1998-02-18									
; PRIOR APPLICATION NUMBER: US 60/094,190									
; PRIOR FILING DATE: 1998-07-27									
; NUMBER OF SEQ ID NOS: 33142									
; SEQ ID NO 15459									
; LENGTH: 468									
; TYPE: DNA									
; ORGANISM: Pseudomonas aeruginosa									
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; Sequence 15280, Application US/09252991A									
; Patent No. 6551795									
; GENERAL INFORMATION:									
; APPLICANT: Marc J. Rubenfield et al.									
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS									
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS									
; FILE REFERENCE: 107196.136									
; CURRENT APPLICATION NUMBER: US/09/252,991A									
; CURRENT FILING DATE: 1999-02-18									
; PRIOR APPLICATION NUMBER: US 60/074,788									
; PRIOR FILING DATE: 1998-02-18									
; PRIOR APPLICATION NUMBER: US 60/094,190									
; PRIOR FILING DATE: 1998-07-27									
; NUMBER OF SEQ ID NOS: 33142									
; SEQ ID NO 15280									
; LENGTH: 1014									
; TYPE: DNA									
; ORGANISM: Pseudomonas aeruginosa									
US-09-252-991A-15280									
Query Match									
Best Local Similarity 6.7%; Score 33.4; DB 4; Length 1014;									
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;									
QY	83	CTCCGATAAAGCCAGCGCCCATATTTGCAGGAGGATTGCGCTGCGGTTTGGCGACATTC	142						
DB	842	CGCGACTACGCTGTACCCCGAGGGTTGCGCGAAGCGCAGCGCGCGGCAAGGTCTCT	783						
QY	143	GGATCCCGGAAACGAGCTCTGCAATGACCTGCGCGCGAGGAAGCGAGTGGTGGCAG	202						
DB	782	GGCTTCGCTGAACATGCAGCTCTATCCCGCGCGCGCAAGGGAGCGCGGCGTCTCGA	723						
QY	203	GTTTTAGTCGGGTTTAAGCGTTCGACAGGCGAGTGGTGACAAAGACGCTAGTCTGGGG	261						
DB	722	GCTGGCGGTGGGTTGCTGTGTTGCTCATGCCGAGGGGTGCATCTTTCTCCAGTGGCGG	664						
RESULT 5									
US-09-252-991A-15508									
; Sequence 15508, Application US/09252991A									
; Patent No. 6551795									

GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15508
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15508

Query Match 6.7%; Score 33.4; DB 4; Length 1842;
Best Local Similarity 49.2%; Pred. No. 0.38;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 83 CTCGATAAGCAGCGCCCATATTTGCAGGGAGGAGTCCCTGCGGTTTGGCGCATTC 142
Db 291 CGCGACTACGCTGTACCCCGAGGGTTGGCGGAAGCGGCGCGCGGCGAGTCTCT 350
QY 143 GGATCCCGAACCAGCTCTGCAATGACCTGCGCGCGGAGGAGCGAGTGGTGGCAG 202
Db 351 GGCTTCGCTGAACATGAGCTCTATCGCGCGCGCGGAGGCGCGGCGGCTGTCTGA 410
QY 203 GTTTTAGTGGGGTTTAAAGCGTTGCGAGGCGAGTGTGACAAAGCGCTAGTCTGGGG 261
Db 411 GCTGGCGTGGGGTTGCTGCTGCTCATGCGGAGGCGTGCATTTCTCCAGTGGCGG 469

RESULT 6

US-09-489-039A-2499/c
; Sequence 2499, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2499
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2499

Query Match 6.5%; Score 32.4; DB 4; Length 831;
Best Local Similarity 53.1%; Pred. No. 0.55;
Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 161 CTGCAATGACCTGCGCGCGGAGGAGCGAGGTGGTGGCAGGTTTATGTCGGGTTAA 220
Db 199 CCGAAGATCTCGTGCCCGGTGAGGAGCGGCGGAGCGGCGGCTATCGTTTCAG 140
QY 221 GCGTTGCGAGCGAGTGTGAGCAAGACGCTAGTCTGGGAGCGGAACCATTTAGTC 280
Db 139 TCATCGCGAGCTGGTGTGGGGTTAATCACTTGTATACGAACGGAACATCAGGACTC 80
QY 281 ATCTTGGCAG 290
Db 79 CTTGTGGCG 70

RESULT 7

US-09-134-000C-348/c
; Sequence 348, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 348
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-348

Query Match 6.2%; Score 31.2; DB 4; Length 732;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 78; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 303 TCTGAGGCGATAGATGGTTTGTCTGATTTTACAAATGATTTTTCACAAAAATAAC 362
Db 688 TCAACATGCGACAGAAAGGTGTCTACGTGTGTTTGTCTTTTGCCTTTGCGCAACGCGAC 629
QY 363 ACTTGTCTGACCACATTTTCGGACATAATCGGCGATTAATTAAGGTGAACAAAGGAAT 422
Db 628 CATTAAATGAATCAATTTCTGTGAGACGATGATTTTAAATTAATCTTGATACATAGAG 569
QY 423 CCGGGCACAGCTCTTGTCTGATTTTCTGAGTCTCT 458
Db 568 GATAGTGCAGCAATGCCATTGGATCATAGTTT 533

RESULT 8

US-09-976-594-673/c
; Sequence 673, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 673
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 231840.1
US-09-976-594-673

Query Match 6.2%; Score 31; DB 4; Length 1825;
Best Local Similarity 55.0%; Pred. No. 2.5;
Matches 61; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 303 TCTGAGGCGATAGATGGTTTGTCTGATTTTACAAATGATTTTTCACAAAAATAAC 362
Db 1770 TGTCCAAGTTTCAGATTAAGTTTGGTAGAATAAAGTCTGAAATTTCAAAATTAATTAG 1711
QY 363 ACTTGTCTGACCACATTTTCGGACATAATCGGCGATAATTTAAAGGTGTA 413
Db 1710 AAATGTAGTCTCAATATTATCATACATAACCTAAATATTATTGTTGTGTA 1660

RESULT 9

US-09-134-000C-2226
; Sequence 2226, Application US/09134000C
; Patent No. 6617156
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58...2523
; US-08-684-932A-37
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58...2523
; US-08-684-932A-37
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2226
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-2226

Query Match 6.2%; Score 31; DB 4; Length 2163;
Best Local Similarity 64.8%; Pred. No. 2.8;
Matches 46; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 310 GGCATAGATTGGTTTGGCTCGCATTTACAAATGATTTTTCACAAAATAACACTTGGT 369
DB 859 GGGATATATTTTGTATTAATGGTTAACTATTCTATTACTGACAATAATGCTCTTGT 918
QY 370 CTGACCACATT 380
DB 919 CTAATCTCTT 929

RESULT 10

US-08-684-932A-37/c
; Sequence 37, Application US/08684932A
; Patent No. 6403304
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: HUMAN OSTEOCLAST-SPECIFIC AND -RELATED
; TITLE OF INVENTION: DNA SEQUENCES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,932A
; FILING DATE: 19-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-02FM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2640 base pairs
; TYPE: nucleic acid

Query Match 6.2%; Score 31; DB 4; Length 2640;
Best Local Similarity 49.1%; Pred. No. 3.1;
Matches 82; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 56 AGAGAGCCACACCATTTCCGATTTCCGATTAAGCCAGCGCCATATTTGCAGGA 115
DB 1378 AGAAAGTCTGCCAGATCTGTTCTCGCGGCTTTACAGCCGGTCTCGGCAAGA 1319
QY 116 GGATTCGCTCGGTTTGGGACATTCGATCCCGGACACAGCTCTGAAATGACCTGG 175
DB 1318 CCATGGCCAGGCGAAGAGAAACATGAGCAGCCCGTGGCCCATCCCCGAACATCAG 1259
QY 176 CGCCGAGGAAGCGAGGTGGTGCGCAGGTTTTAGTGGGGTTTAAAGC 222
DB 1258 CAACAGGAAGGGAGGTGATGATGTTAGGGAGCGGGTTGACC 1212

RESULT 11

US-09-016-434-1094/c
; Sequence 1094, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1094:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1245045
; US-09-016-434-1094

Query Match 6.2%; Score 31; DB 4; Length 2655;
Best Local Similarity 49.1%; Pred. No. 3.1; Mismatches 85; Indels 0; Gaps 0;
Matches 82; Conservative 0;

QY 116 GGATTCGCTGGGTTTGGCGACATTCGATCCCGGAACACGCTCTGCAATGACCTGGC 175
DB 1318 CCATGCCAGGCGGAAGAGGAACATGAGCAGCCCGTGGCCACATCCCGAATCAGAG 1259

QY 176 CGCCGAGGGAACGAGGTGGTGGCAGGTTTGTAGTGGGGTTTAAAGC 222
DB 1258 CAAACAGGAAGGGAAGGTGATGATGGTGTAGGAGGCGGGTTGACC 1212

QY 56 AGAGAGCCACACATTCGATTTCCGCTCCGATAAAGCCAGCGCCATATTGAGGGA 115
DB 1378 AGAAGTCTGCAGATCTGTTCTGCGCGCTTTCACAGCCGCTGCTCCGCAAGGA 1319

QY 116 GGATTCGCTGGGTTTGGCGACATTCGATCCCGGAACACGCTCTGCAATGACCTGGC 175
DB 1318 CCATGCCAGGCGGAAGAGGAACATGAGCAGCCCGTGGCCACATCCCGAATCAGAG 1259

QY 176 CGCCGAGGGAACGAGGTGGTGGCAGGTTTGTAGTGGGGTTTAAAGC 222
DB 1258 CAAACAGGAAGGGAAGGTGATGATGGTGTAGGAGGCGGGTTGACC 1212

RESULT 13
US-10-027-983-11/c
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (195242)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature

RESULT 12
US-09-023-655-916/c
; Sequence 916, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 916:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1245045
; US-09-023-655-916

Query Match 6.2%; Score 31; DB 4; Length 2655;
Best Local Similarity 49.1%; Pred. No. 3.1; Mismatches 85; Indels 0; Gaps 0;
Matches 82; Conservative 0;

QY 56 AGAGAGCCACACATTCGATTTCCGCTCCGATAAAGCCAGCGCCATATTGAGGGA 115
DB 1378 AGAAGTCTGCAGATCTGTTCTGCGCGCTTTCACAGCCGCTGCTCCGCAAGGA 1319

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; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (223981)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232259)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(2366651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
; US-10-027-983-11

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Query Match
Best Local Similarity 6.1%; Score 30.6; DB 4; Length 392000;
Matches 78; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 266 AAACATATTGAGTCATCTTGCGAGCATGCACAAATCTGCGAGGCATAGATTGGTTT 325
DB 253273 AACCTAAAAGCAATCATTTAGCCAAAAGGGGAGATGGGTAGGGGAAAAGATGAAAA 253214

QY 326 GCTCGATTTACAATGTGATTTTTCACAAAAATAACACTTGGTCTGACCAATTTTCGG 385
DB 253213 GAAGGGTAATGTACAAATATTTCATCTCATCAAGTCACCAATAGATATGTCCAA 253154

QY 386 ACATAATCGGCATATTTAAAGGTCTACAAAGGAAT 422
DB 253153 AGTTGATAAGTCAAAATATAGGTTTATTATAGGTAT 253117

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RESULT 14
US-09-566-921-54
; Sequence 54, Application US/09566921
; Patent No. 668288
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138

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; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inceyte ID No. 6682888 331485.3
; US-09-566-921-54

```

```

Query Match
Best Local Similarity 6.1%; Score 30.4; DB 4; Length 5722;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 294 ATGCACAAATTCGAGGCATAGATTGGTTTCTCGATTTCAGATTCAATGTGATTTTCAAC 353
DB 2472 ATGTAGATTTAGGATGCCCTATTGCTGCTTTCTAGATTAAATGAGATCTTTGAACC 2531

QY 354 AAAAATACACTTGGTCTGA 373
DB 2532 AGGAGGAGATCTTCATCTGA 2551

```

```

RESULT 15
US-09-441-346A-3
; Sequence 3, Application US/09441346A
; Patent No. 6242588
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fiddington, Christopher S.
; APPLICANT: Ellsworth, Jeff L.
; TITLE OF INVENTION: TESTIS-SPECIFIC GLYCOPROTEIN ZPEP10
; FILE REFERENCE: 98-34
; CURRENT APPLICATION NUMBER: US/09/441,346A
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,216
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zpep10
; OTHER INFORMATION: polypeptide of SEQ ID NO:2
; NAME/KEY: variation
; LOCATION: (1)....(426)
; OTHER INFORMATION: Each N is independently any nucleotide.
; US-09-441-346A-3

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Query Match
Best Local Similarity 6.0%; Score 30; DB 3; Length 426;
Matches 51; Conservative 37; Mismatches 110; Indels 0; Gaps 0;

QY 6 AGCCAGGTAGCGGTGTAACCCACCGTTTCGGCAACAATGACGGCGAGAGGCCA 65
DB 88 MGNVTGNCNMGNTNTGYWSNCARATGGARCNMGNCARARGARTGGNGCWNSCN 147

QY 66 CCACATTGCGATTTCCGCTCCGATTAAGCCAGCCCATATTTGCAGGAGGATTCGCT 125
DB 148 GAYTTYWSNGCNTTYGCTNYNGAYGARTWNSNATGAAYAAAGTACNAGARARACNCAY 207

QY 126 GCGGTTTGGCGACATTCGGATCCCGGAAACCAGCTCTGCAATGACCTCGCGCGGAGGA 185
DB 208 MGNGTNTNMGNTNATGGNGGWSNACNACNTTNTAYAYTGYWSNACNTGYAARGGN 267

QY 186 AGCCAGGTGGGTGGCAGG 203
DB 268 ACNGAGTNTWSNTGYTGG 285

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us-09-987-763-7.rni

Fri Aug 6 10:32:28 2004

Job time : 71 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 11:50:56 ; Search time 2380 Seconds

(without alignments)
6273.567 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcgcc.....atcaggaaagtggaatcgaaa 500

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_estum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.4	8.5	1018	12	BG684402
C 2	41.2	8.2	1201	13	BX394291
C 3	40.0	8.0	1610	28	AF057117
C 4	38.6	7.7	1201	13	BX381961
					BG684402 602636153
					BX394291 BX394291
					AF057117 AF057117
					BX381961 BX381961

C 5	7.6	743	28	BZ146910
C 6	7.6	1221	29	AG058113
C 7	7.6	835	14	CK203550
C 8	7.4	682	28	AZ420591
C 9	7.3	1201	9	AL519510
C 10	7.3	1215	28	CC285387
C 11	7.3	570	28	BH428607
C 12	7.3	672	29	AG167527
C 13	7.3	725	28	BZ514039
C 14	7.3	732	28	BZ453110
C 15	7.3	837	28	AZ129743
C 16	7.2	885	13	BX425603
C 17	7.2	417	13	BX637673
C 18	7.2	456	9	AI722358
C 19	7.2	755	28	BZ061578
C 20	7.2	1201	13	BX376774
C 21	7.1	1201	13	BX340397
C 22	7.1	685	29	AG183454
C 23	7.0	1252	28	CC324229
C 24	7.0	635	29	CE015870
C 25	7.0	345	10	BF714393
C 26	7.0	559	28	AQ061172
C 27	7.0	663	9	AV972628
C 28	7.0	916	29	CNS04841
C 29	7.0	1029	29	CNS016QV
C 30	7.0	1201	13	BX416614
C 31	6.9	674	13	BW010388
C 32	6.9	748	28	BZ341132
C 33	6.9	893	14	CK245533
C 34	6.9	1201	13	BX353189
C 35	6.9	331	10	BF231100
C 36	6.9	524	12	BG097296
C 37	6.9	1201	13	BX399745
C 38	6.9	1201	13	BX419736
C 39	6.8	237	10	BB007989
C 40	6.8	338	10	BB519478
C 41	6.8	555	14	CA276805
C 42	6.8	565	12	BQ018827
C 43	6.8	605	13	BQ857538
C 44	6.8	684	29	AG095157
C 45	6.8	1101	29	CNS00F1J

ALIGNMENTS

RESULT 1
BG684402/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG684402 1018 bp mRNA linear EST 01-MAY-2001
602636153F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4763989 5',
mRNA sequence.

BG684402

BG684402.1 GI:13915799

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1018)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM1620 row: i column: 14

High quality sequence stop: 4.

[illegible]

	db	776	AAMHNCAMTTT	KAMAMBAATTBOMTTKMTTMTTKMMCTHTKCTKNKKVMHKKKKK	835
	QY	352	ACAAATAAACACT	TGTGTCACCAACATTTTTCCGCACATAATCGGGCATAATTAAAGGTGT	411
	db	836	MHBACAMTKWNT	TKKKMKMTWCMCKKKKKKANAKMAMKKKKKKKMAHAMAMMKKG	895
	QY	412	AACAAAGAATCC	GGGCACAAGCTCTTGCTGAATTTCTGAGCTGCTTTGTGGGTGTGCCG	471
	Db	896	CMFKCKMHKKKK	NNKAMMMKKKKKKKKKBKNMBKKKAMAMNDHKKCKCKKCAAK	955
	QY	472	GTTAGGGAATC	AGGAAGTCGGATCGAAA	500
	Db	956	MAAWKAHAHA	ACMNCCAKKKKKKKKKAACA	984

AF057117 1610 bp DNA linear GSS 21-FEB-2001
 AF057117 Human Homo sapiens genomic clone 016H probe, genomic
 survey sequence.
 AF057117
 AF057117.1 GI:3142424
 GSS.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1610)
 Janer, M. and Geraghty, D. E.
 The human major histocompatibility complex: 42,221 bp of genomic
 sequence, high-density sequence-tagged site map, evolution, and
 polymorphism for HLA class I
 Genomics 51 (1), 35-44 (1998)
 98360090
 9693031
 Contact: Janer M
 Geraghty Lab
 Fred Hutchinson Cancer Research Center
 1100 Fairview Ave., D2-100, Seattle, WA 98109-1024, USA
 Email: geraghty@fhcrc.org
 Class: unpub.
 Comment:

```

CLASS: unknown.
EATURES
  source
    Location/Qualifiers
      1..1610
        /organism="Homo sapiens"
        /mol_type="Genomic DNA"
        /db_xref="taxon:9606"
        /map="6p21.3; HLA Class I region"
        /clone="016H probe"
        /clone_lib="Human"
      RIGIN
      Query Match 8.0%; Score 40; DB 28; Length 1610;
      Best Local Similarity 49.3%;

```

QY 265 GAAACCATATTGAGTCATCTTGGCAGAGCATGCACAATTTCTCGAGGGCATAGATTGTGTTT 324
 :
 Db 959 KMKMKNKMGVNNKTKMMMBKKMNKNKNMKGKYVMGMKKXNMKKXNMKNMKNMKNMKGKGMK 900
 :
 QY 325 TGCTCGATTTTACAATGTGAATTTTCAACAAAAATAACACTTGCTCTGACCACATTTTCG 384
 :
 Db 899 KGNMVVKKNMKNMKGKKTGKTKKKKKNNHMKTKTMNMMKKKKKKKKKKKKKKNNMVGKMGK 840
 :
 QY 385 GACATAATCCGGCATAAATTAAGGTGTAAACAAAAGAATCCGGGCACAAGC 434
 :
 Db 839 KMGGKKVMKGMKNMKNMKGKGBKCKCWVRKMNMNMKGKGMGKKMMNMGM 790
 :

```

RESULT 5
BZ146910/c
LOCUS      BZ146910              743 bp       DNA          linear      GSS 11-OCT-2002
DEFINITION CH230-319H2.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-319H2, genomic survey sequence.
ACCESSION  BZ146910
VERSION    BZ146910.1 GI:23787857
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
ORGANISM   Rattus norvegicus [Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.]
REFERENCE  1 (bases 1 to 743)
AUTHORS   Zhao,S., Shetty,J.J., Shatsman,S., Teagaye,G., Geer,K., Shvartsbeyn,A., Gebregorjais,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL   Unpublished (1999)
COMMENT   Other_GSSs: CH230-319H2.TV
           Contact: Shaying Zhao
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: szhaow@tigr.org
           Clones are derived from the rat BAC library CHORI-230
           (http://www.chori.org/bacpac/rat230.htm). For BAC library
           availability, please contact Pieter de Jong (pdejong@mail.cho.org).
           Clones may be purchased from BACPAC Resources
           (http://www.chori.org/bacpac/orering/information.htm). BAC end
           page: http://www.tigr.org/tldb/bac\_ends/rat/bac\_end\_intro.html
           Plate: 319 row: H column: 2
           Seq primer: SP6
           Class: BAC ends.

FEATURES             Location/Qualifiers
     source            1..743
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SSHsd/MCN"
                     /db_xref="taxon:10116"
                     /clone="CH230-319H2"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
                           CHORI-230 Rat (BN/SSHsd/MCN) BAC library produced by
                           Pieter de Jong"

ORIGIN
Query Match               7.6%; Score 38; DB 28; Length 743;
Best Local Similarity    52.5%; Pred. No. 3;
Matches                  83; Conservative                75; Indels        0; Gaps         0

QY 318 TTGCGTTTTCGATTTACAATGTGAATTTTTCAACAAAAATAACACTTGCTCTGACAC 377
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 TTGCGATTACTAATATATPAAGACACTTCTCATTTGGTTGTTTCTGCTTACTGCCGG 482
|||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Ov 378 ATTTTCGGACATATCCGGCATAAATTAAGGTGTAACAAGGATCCGGGCACAAGCTCT 437

```

Db 481 AATTCATGACATATTCGTGAGTCTCTCTGTTGTAACACACTCAGAAAAACAACACT 422
 QY 438 TCGTGTATTTCTGAGCTGCTTTGTGGGTGTGTCGGTTA 475
 Db 421 GTAGAAGTTAGTCTACTGCTCTCTTTGTTGTCTAGTTA 384

RESULT 6
 AG058113
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: PTB-044012.F, genomic survey sequence.
 AG058113
 VERSION AG058113.1 GI:16595574
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of Library PTB
 Unpublished
 2 (bases 1 to 1221)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB. This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: -21M13
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1. .1221
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-044012.F"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES
source

ORIGIN

Query Match 7.6%; Score 38; DB 29; Length 1221;
 Best Local Similarity 49.2%; Pred. No. 3.6;
 Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 QY 49 GACGCGGAGAGAGCCACCATTCGATTCCTCGATTAAGCCAGCGCCCATATTT 108
 Db 874 GCCCGGAGGAGGCCCGCCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 933
 QY 109 GCAGGAGGATTCGCTGCGGTTTGGCGACATTCGATCCCGGAGACAGCTCTGCAATG 168
 Db 934 GCGCGGCGGACG 993
 QY 169 ACCTGCG 228
 Db 994 GCG 228
 QY 229 AGCGGAGTGTGAGCAAAAG 247
 Db 1054 GCGCGCGCGCGCGCGCGAG 1072

RESULT 7
CK203550
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE
AUTHORSTITLE
JOURNAL

COMMENT

CK203550 835 bp mRNA linear EST 08-DEC-2003
 FGAS012081 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
 aestivum cDNA, mRNA sequence.
 CK203550
 CK203550.1 GI:39565940
 EST.
 Triticum aestivum (bread wheat)
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.
 1 (bases 1 to 835)
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
 Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
 Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada
 Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [102,729].
 Plate: L3C117 row: C column: 10.

FEATURES

source

1. .835
 Location/Qualifiers
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
 control, cold-acclimated and salt stressed wheat cultivar
 Norstar. 7 mRNA populations were combined before
 constructing the library; 7 day non-acclimated roots, 1,
 23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
 hours and 6 hours treated roots with 200mM NaCl.
 Non-acclimated and cold-acclimated plants were grown in
 vermiculite while salt stressed plants were grown
 hydroponically. First strand synthesis in this library was
 done in the presence of methylated dCTP thereby protecting
 from internal cleavage with NotI."

ORIGIN

Query Match 7.6%; Score 37.8; DB 14; Length 835;
 Best Local Similarity 57.0%; Pred. No. 3.6;
 Matches 69; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 QY 339 TGTGATTTTTCACAAAATAACACTTGGTCTGACCATTTTCGACATAATCGGCA 398
 Db 445 TGTTCGTTATTCAAGAGATCAACTTCTTGACCTGCGCAAGATTACTGATGTAACCGACA 504
 QY 399 TAATTAAGGTGTACAAAGGAATCCGGCACAAGCTTCTGCTGATTTCTGAGCTGTT 458
 Db 505 AATCTGAGGCTTCAGCAAGAAATTGAAGCAGAGCTTCATGTCGATCAGATCAGCTGGT 564
 QY 459 T 459
 Db 565 T 565

RESULT 8
 AZ420591/c

Fri Aug 6 10:32:29 2004

LOCUS AZ420591 682 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0198D05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0198D05 R, genomic survey sequence.

ACCESSION AZ420591 GI:10544604

VERSION GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: D column: 05

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 682.

Location/Qualifiers

1. 682

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0198D05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pW42 (G114732114[gb]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 7.4%; Score 36.8; DB 28; Length 682;

Best Local Similarity 55.5%; Pred. No. 6.9;

Matches 71; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 289 AGAGCATGCACAAATCTCGAGGCGCATAGATTGGTTTCTCGATTACATCTGATTTT 348

DB 630 AGAGCTTGTGGTCTTCAAGATATGATTTCATTTGGCCCAATAAAAAATGTTTAT 571

QY 349 TCAACAAAAATACACTTGGTCTGACCACATTTTCGGACATATCGGCGCATATTAAGG 408

DB 570 TTTATAAAGATATTTCATAGATTTCCTTAGCTTTAGCCGACGATCTATCTAGAAATTAACA 511

QY 409 TGTAAACA 416

DB 510 CATGAAAA 503

RESULT 9

AL519510

LOCUS

DEFINITION

AL519510 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens

CDNA clone CSODB004YA16 5-PRIME, mRNA sequence.

ACCESSION

AL519510

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Feb 13, 2001 this sequence version replaced gi:12783003.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 781.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODB004BA08QPI&cluster=781.f. Contact :

Feng Liang Email: fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODB004BA08QPI.

Location/Qualifiers

1. 1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODB004YA16"

/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 7.3%; Score 36.6; DB 9; Length 1201;

Best Local Similarity 27.7%; Pred. No. 9.7;

Matches 74; Conservative 74; Mismatches 118; Indels 1; Gaps 1;

QY 11 GGTAGCGGCTTAACCCACACCGGTTTCGGCAACATGACGCGGAGAGCCACACA 70

DB 544 SSSSTSSSTATASASTSTSSASATSTSSASAASTTTSSSSSTSTSSSSASSTSA 603

QY 71 TTGCGATTCCGTCGATTAAGCCAGCCGCCATATTG-CAGGAGGATTTCGCTCGG 129

DB 604 SASASSSTSTSSSTSTSSATSSSSSSSTSSSSSTSSSSSTSSSTSSSTSS 663

QY 130 TTGGCGACATTCGGATCCCGAACACGCTCTCAATGACCTTCGGCGCCGAGGAGCG 189

DB 664 SSSSTSSASSSSAGTSTSSASSSSASATTTSTSSASSAATSTSTSSGAGATG 723

QY 190 AGTGGTGGCGCAGGTTTGTAGTCGGGTTTAAAGCGTTGCCAGCGGAGTGTGACCAAGAC 249

DB 724 ATGTGAGGCGTGTGCGGAGTGGGTGTTGGATGGGAGGAGTGGGAGGAGG 783

QY 250 GCTAGTCTGGGAGCGAAACCATATTG 276

DB 784 GATAGTGGAGGGGGTGAAGAAGATTG 810

FEATURES

source

```

RESULT 10
CC285387/c
LOCUS
DEFINITION
  CC285387
  1215 bp DNA linear GSS 13-MAY-2003
  Genomic survey sequence.
  CH261-28H5, Sp6.1 CH261 Gallus gallus genomic clone CH261-28H5,
  CC285387
  CC285387.1 GI:30653842
  GSS.
  Gallus gallus (chicken)
  Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
  1 (bases 1 to 1215)
  Krenitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
  Warren, W., Graves, T., Mardis, E. and Wilson, R.
  Gallus gallus BAC End Reads
  Unpublished (2003)
  Contact: Richard K. Wilson
  Genome Sequencing Center
  Washington University School of Medicine
  Email: submissions@watson.wustl.edu
  Insert Length: 182000 Std Error: 0.00
  Seq primer: Sp6 ATTATGTCACACTATAG
  Class: BAC ends
  High quality sequence start: 195
  High quality sequence stop: 386.
  Location/Qualifiers
    1..1215
      /organism="Gallus gallus"
      /mol_type="genomic DNA"
      /strain="Red Jungle Fowl"
      /db_xref="taxon:9031"
      /clone="CH261-28H5"
      /sex="female"
      /cell_line="UCD001, inbred 256"
      /clone_lib="CH261"
      /notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
      CH261 Female Chicken library - For library and clone
      ordering information: http://www.chori.org/bacpac"

ORIGIN
Query Match 7.3%; Score 36.6; DB 28; Length 1215;
Best Local Similarity 52.3%; Pred. No. 9.7;
Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 331 ATTCAATGTCATTTTTCACAAATAAATACACTGGTCGACCAATTTTCGGACATA 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ATTCACAGTTTATTTTAAACAAAGAAAGATAGAAATACTTACTGTGTTTCAATTA 259

QY 391 ATCGGGCATAATTAAGGTGTAACAAAGGAATCCGGGCACACAGCTTCTGCTGATTTCTG 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db TTCTCAGAACATTCAGCGGTAAAGAAAGAAATCAATGACAGATGTTGAGGGCTTCTTTA 199

QY 451 AGCTGCTTTGCGTTGTCGGTTAGCGGAATCAG 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db TTTTGCTATTGTTGTTGTAAGGAAGGAGACAG 164

RESULT 11
BH428607
LOCUS
DEFINITION
  BH428607
  570 bp DNA linear GSS 12-DEC-2001
  BOHS548TF BOHS Brassica oleracea genomic clone BOHS548, genomic
  survey sequence.
  BH428607
  BH428607.1 GI:17614328
  GSS.
  Brassica oleracea
  Brassica oleracea
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

ORIGIN
Query Match 7.3%; Score 36.6; DB 28; Length 570;
Best Local Similarity 56.8%; Pred. No. 8.6;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 233 GAGTGGTGACAAAGACGCTAGTCTGGGAGCGGAACCAATATTGAGTCATCTTGGCAGAG 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GAGAGCTGGTTTAAAGCAGAAACCTGTGGAGAGAGAGCTGTAGAGTCGTTAGGGAGAA 341

QY 293 CATGCACAATTCGACGGGCATAGATTGTTTTCGATTTTCAATGATGATTTTTC 350
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Db 342 GATGAAGAGGTGGGGTTACCATTAAGACTTTGTCTGTGTAAGAGATAGTAATTGGTTTC 399

RESULT 12
AG167527/c
LOCUS
DEFINITION
  AG167527
  672 bp DNA linear GSS 09-JAN-2002
  Pan troglodytes DNA, clone: RP43-035024.T7, genomic survey
  sequence.
  AG167527
  AG167527.1 GI:16697205
  GSS.
  Pan troglodytes (chimpanzee)
  Pan troglodytes
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
  Totoki, Y., Watanabe, H. and Sakaki, Y.
  BAC end sequences of Library RPCI-43
  Unpublished
  2 (bases 1 to 672)
  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
  Totoki, Y., Watanabe, H. and Sakaki, Y.
  Direct Submission
  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
  (E-mail:chimps@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
  Tel:81-45-503-9111, Fax:81-45-503-9170)
  Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
  end was generated during the R&D process and may have higher chance
  of clone tracking errors.
  PRIMERS
  Sequencing: T7
  LIBRARY
  Vector : pBACe3.6
  R.Site 1 : EcoRI

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233 GAGTGGTGACAAAGACGCTAGTCTGGGGAGCGAAACCATATTTGAGTCATCTGGCAGG

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ehrhartoideae; Oryzae; Oryza.
1. (bases 1 to 837)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 21
High quality sequence stop: 704.

FEATURES
source

1..837
Location/Qualifiers
1..837
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:3994"
/clone="OSJNB0068C15r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CGI Rice BAC Library (EcoRI)"
/note="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9%. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match
Best Local Similarity 7.3%; Score 36.4; DB 28; Length 837;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY	280	CATCTTGGCAGACATGACAAATTCGAGGCGATAGATTTGGTTTCGATTTTACAAAT	339
Db	582	CACATAGCCAAACCATTCAGTATATCCAGGACATAGTTTATCACAATATTTTAAAT	523
QY	340	GTGATTTTTCACAAAAATAACACTTGGTCTGACCAATTTTCGACATATCGGGCAT	399
Db	522	AATATTATTTTAAAAAAATTTTTCAGTTACCAATACACATAATAAATAATTCCTAAGT	463
QY	400	AATTAAAGGTGTAAACAAAGGAA	421
Db	462	AAATTAAGTAGTAGAAGGAA	441

Search completed: August 4, 2004, 13:23:57
Job time : 2385 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 12:44:02 ; Search time 318 Seconds
(without alignments)
7709.340 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagcaggttagggc.....atcaggaagtggaatcgaaa 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	490.4	98.1	3309400	9	US-09-738-626-1
3	264	52.8	1776	9	US-09-738-626-3211
4	37.6	7.5	594	13	US-10-142-426-10
5	37.6	7.5	594	15	US-10-123-155-10
6	37.6	7.5	594	15	US-10-146-731-10
7	37.6	7.5	594	15	US-10-140-472-10
8	37.6	7.5	594	15	US-10-141-761-10
9	37.6	7.5	594	15	US-10-142-885-10
10	37.6	7.5	594	16	US-10-158-790-10
11	37.6	7.5	594	16	US-10-137-871-10
12	37.6	7.5	594	16	US-10-140-923-10
13	37.6	7.5	594	16	US-10-141-756-10
14	37.6	7.5	594	16	US-10-141-759-10

15	37.6	7.5	594	16	US-10-140-805-10	Sequence 10, Appl
16	37.6	7.5	594	16	US-10-140-864-10	Sequence 10, Appl
17	36.2	7.2	1053	13	US-10-282-122A-29887	Sequence 29887, A
18	34.8	7.0	1508	16	US-10-369-493-44140	Sequence 44140, A
19	34.8	7.0	152331	14	US-10-095-407-16	Sequence 16, Appl
20	34.2	6.8	32591	16	US-10-085-117-187	Sequence 187, App
21	34	6.8	433	13	US-10-424-599-4852	Sequence 4852, Ap
22	33	6.6	1328	13	US-10-027-632-123211	Sequence 123211,
23	33	6.6	1328	16	US-10-027-632-123211	Sequence 123211,
24	33	6.6	2278	13	US-10-424-599-117564	Sequence 117564,
25	32.8	6.6	32191	10	US-09-764-891-8965	Sequence 47080, A
26	32.2	6.4	335	13	US-10-085-783A-4787	Sequence 8965, Ap
27	32.2	6.4	335	16	US-10-242-538A-4787	Sequence 4787, Ap
28	32.2	6.4	624	13	US-10-027-632-223801	Sequence 223801,
29	32.2	6.4	624	16	US-10-027-632-223801	Sequence 223801,
30	32.2	6.4	637	13	US-10-027-632-250227	Sequence 250227,
31	32.2	6.4	637	16	US-10-027-632-250227	Sequence 250227,
32	32.2	6.4	2632	15	US-10-198-846-11330	Sequence 11330, A
33	32.2	6.4	304905	13	US-10-271-416-1	Sequence 1, Appl
34	32.2	6.4	577	9	US-09-864-761-14811	Sequence 14811, A
35	32	6.4	701	13	US-10-027-632-236918	Sequence 236918,
36	32	6.4	701	16	US-10-027-632-236918	Sequence 236918,
37	32	6.4	701	16	US-10-027-632-236918	Sequence 236918,
38	32	6.4	701	16	US-10-027-632-236918	Sequence 236918,
39	32	6.4	796	17	US-10-437-963-40252	Sequence 236919,
40	32	6.4	998	13	US-10-027-632-258465	Sequence 258465,
41	32	6.4	998	16	US-10-027-632-258465	Sequence 258465,
42	32	6.4	3186	13	US-10-027-632-114364	Sequence 114364,
43	32	6.4	3186	16	US-10-027-632-114364	Sequence 114364,
44	32	6.4	344548	13	US-10-087-192-334	Sequence 334, App
45	32	6.4	344548	13	US-10-087-192-334	Sequence 334, App

ALIGNMENTS

RESULT 1

US-09-987-763-7
; Sequence 7, Application US/09987763
; Publication No. US2003001753A1
; GENERAL INFORMATION:
; APPLICANT: Rayapati, P. John
; APPLICANT: Crafton, Corey M.
; TITLE OF INVENTION: Nucleotide Sequences for Transcriptional Regulation in
; TITLE OF INVENTION: Corynebacterium glutamicum
; FILE REFERENCE: 1533.1940002
; CURRENT APPLICATION NUMBER: US/09/987,763
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,219
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-987-763-7

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Gaps	0;						
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181	AGGGAAGCGAGGTGGGTGGCAGGTTTTAGTCCGGGTTTAAGCGTTGCCAGCGAGTGGTG	240
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241	AGCAAGAAGCGTAGTCTGGGAGCGAAACCAATATTAGTCACTCTGGCAGAGCATGCACA	300
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301	ATTCTCGAGGCGATAGATTGGTTTGTCTCGAATTTACAAATGTGATTTTTTCAACAAAAATA	360
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361	ACACTTGGTCTGCACACACATTTTCGGACATAATTCGGGCATAATTAAGGTGTAAACAAAGGA	420
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RESULT 2
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1

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[illegible]

152 GGCCTGCGGTTTGGCGACATTCCGATCCCGGAAGCTAGCTCTGCAATGACCTGCGCGCG 93

181 AGGAAAGCAGCTGGTGGCAGGTTTTAGTCGGGTTTTAAGCGTTTGCCAGGCGAGTGGTG 240

92 AGGAGCGCAGTGGTGGCAGGTTTTAGTCGGGTTTTAAGCGTTTGCCAGGCGAGTGGTG 33

241 AGCAAGACGCTAGTCTGGGAGCGAAACCAT 272

32 AGCAGACGCTAGTCTGGGAGCGAAACCAT 1

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RESULT 4
US-10-142-426-10
; Sequence 10, Application US/10142426
; Publication No. US20040048333A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33081C224
; CURRENT APPLICATION NUMBER: US/10/142,426
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-426-10

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	Query Match	7.5%; Score 37.6; DB 13; Length 594; Best Local Similarity 8.7%; Pred. No. 0.13; Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0
Qy	7	GCACGGTTAGCGGCTGTAACCCACACACGGTTTCGGCAACAATGACGGCAGAGAGCCAC 66
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Qy	67	CACATTGCGATTTCGCTCCGATAAAGCCAGCGCCCATATTTGCAGGGAGGATTCGCCTG 126
Db	289	YARRDSPYDPKYRSPSSSSSRSRSRSPPTGRIEBKTTTFISFGSDEAAAAA 348
Qy	127	CGGTTTGGCGACATTCCGATCCCGGAACACAGCTCTGCAATACCTGCGCGCCAGGGAA 186
Db	349	SGVITCKPAPPQPGPAPGRNASRRSSSSSSSSSSASRTSSSRSSSSSRSRGGGY 408
Qy	187	GCAGGTGGTGGCAGGTTTATGTCGGGTTTAAAGCTTCCACGGCGAGTGTGAGCAA 246
Db	409	YRSGRHARSRSWSRSRSRRYRSRSRGRHSGGSRDGHYRSRSPARRGGYGRRR 468
Qy	247	GACGCTAGTCTGGGAGCGAAACCA 271
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RESULT 5

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US-10-123-155-10
; Sequence 10, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DePorge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-10

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[illegible]

RESULT 6
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

Db 229 GMADGDFVRLMKDKEAEAIKHALEBEKAMYSGRSRRRRREFREKLRGRKISPPS 288
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QY 247 GACGCTAGTCTGGGAGCGAAACCA 271
Db 469 SRSRSHGDRYRGRGLRHSSSR 493

RESULT 9

US-10-142-885-10
; Sequence 10, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-885-10

Query Match 7.5%; Score 37.6; DB 15; Length 594;
Best Local Similarity 8.7%; Pred. No. 0.13;
Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0;
QY 7 GCGAGTTAGCGGCTGTAAACCCAGCGTTTCGGCAACATGACGCGGAGAGCCAC 66
Db 229 GMADGDFVRLMKDKEAEAIKHALEBEKAMYSGRSRRRRREFREKLRGRKISPPS 288
QY 67 CACATTGCGATTCCGCTCGGTAAGACGAGCCCATATTTCAGGAGGATTCGCGCTG 126
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QY 127 CGGTTGGCGACATTCGGATCCCGGAACGAGCTCTGCAATGACCTCGCGCGCGAGGAA 186
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Db 409 YRSGRHARSRSWSRSRSTRSRSGRRHSGGSRDGHYRSRSPARRGGYGP 468
QY 247 GACGCTAGTCTGGGAGCGAAACCA 271
Db 469 SRSRSHGDRYRGRGLRHSSSR 493
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US-10-158-790-10
; Sequence 10, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-790-10

Query Match 7.5%; Score 37.6; DB 15; Length 594;
Best Local Similarity 8.7%; Pred. No. 0.13;
Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0;
QY 7 GCGAGTTAGCGGCTGTAAACCCAGCGTTTCGGCAACATGACGCGGAGAGCCAC 66
Db 229 GMADGDFVRLMKDKEAEAIKHALEBEKAMYSGRSRRRRREFREKLRGRKISPPS 288
QY 67 CACATTGCGATTCCGCTCGGTAAGACGAGCCCATATTTCAGGAGGATTCGCGCTG 126
Db 289 YARSDPTDYPYKRSSESSESRSRSTPTGREKTIITFSFGSDEAAAAA 348
QY 127 CGGTTGGCGACATTCGGATCCCGGAACGAGCTCTGCAATGACCTCGCGCGCGAGGAA 186
Db 349 SGVTTCKPAPPQPGGPAFGRNASARRSSSSSSASRTSSRSRSTRSRGGY 408
QY 187 GCGAGTGGTGGCAGGTTTAGTGGGTTTAAAGCTTCCAGCGAGTGGTGAGCAA 246
Db 409 YRSGRHARSRSWSRSRSTRSRSGRRHSGGSRDGHYRSRSPARRGGYGP 468
QY 247 GACGCTAGTCTGGGAGCGAAACCA 271
Db 469 SRSRSHGDRYRGRGLRHSSSR 493

RESULT 11

US-10-137-871-10
; Sequence 10, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.


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Db      289 YARRDSFTYDPYKRSPSESSSRSSRSPPTGREKIIPTISFGGSDDEAAAAAAAAA 348
QY      127 CGGTTTGGCGACATTCCGATCCCGGAACAGACTCTGCAATGACCTGCGCGCGAGGAA 186
      :||| : : : : : : : : : : : : : : : : : : : : : : : :
Db      349 SGVTTCKPPAPPQGGPAPGRNASARRRSSSSSSSSASRTSSRSRSSRSGG 408
QY      187 GCGAGGTGGTGGCAGGTTTACTGCGGGTTTAAAGCTTCCAGCGGAGTGGTGAGCAA 246
Db      409 YRSGRHARSRSRWSRSRSRSSRYSRSGRRHSGGGRDGHYRSRPARRGGYGP 469
QY      247 GAGCTAGTCTGGGAGCGAAACCA 271
Db      469 SRSRSHSGDRYRGRGLRHSSSR 493

RESULT 15
US-10-140-805-10
; Sequence 10, Application US/10140805
; Publication No. US20030207417A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P1330R1C176
; CURRENT APPLICATION NUMBER: US/10/140,805
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-805-10

Query Match 7.5%; Score 37.6; DB 16; Length 594;
Best Local Similarity 8.7%; Pred. No. 0.13;
Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0;

QY      7 GCGAGGTGAGGCTGTAAACCCACCGGTTTCGGCAACAATGACGCGGAGAGGCCAC 66
      :| : : : : : : : : : : : : : : : : : : : : : : :
Db      229 GMAGDGFMRLRKDEAEAKHAKALEEKAMYSGRSRQRREFREKLGRKISPPS 288
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QY      187 GCGAGGTGGTGGCAGGTTTACTGCGGGTTTAAAGCTTCCAGCGGAGTGGTGAGCAA 246
Db      409 YRSGRHARSRSRWSRSRSRSSRYSRSGRRHSGGGRDGHYRSRPARRGGYGP 469
QY      247 GAGCTAGTCTGGGAGCGAAACCA 271
Db      469 SRSRSHSGDRYRGRGLRHSSSR 493

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Search completed: August 4, 2004, 14:28:42
Job time : 323 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 13:25:32 ; Search time 2121 Seconds
(without alignments)
10217.594 Million cell updates/sec

Title: US-09-987-763-7
Perfect score: 500
Sequence: 1 aaaaacagccaggttagcggc.....atcaggaaagtggatcgaaa 500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 3470272 seqs, 21671516995 residues

Word size : 0
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
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- 7: gb.ph.*
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- 9: gb.pr.*
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- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
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- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
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- 27: em.sts.*
- 28: em.un.*
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- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.gv.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	500	100.0	500	6	AX431553	Sequence
C 2	275	55.0	309400	6	AX127153	Sequence
C 3	275	55.0	325651	1	AP005283	Corynebac
C 4	134	26.8	1776	6	AX123295	Sequence
C 5	134	26.8	1776	6	BD165412	Novel pol
6	112	22.4	1084	6	AX763278	Sequence
7	100	20.0	1065	6	AX065003	Sequence
C 8	23	4.6	146505	8	F21M12	Sequence
C 9	21	4.2	816	3	AF302055	Ceratosol
C 10	20	4.0	8729	8	AF076155	Arabidops
C 11	20	4.0	25230	3	U88174	Caenorhabdi
C 12	20	4.0	28577	3	AF000264	Caenorhabdi
C 13	20	4.0	34309	3	CEC05A9	Caenorhabdi
C 14	20	4.0	98535	10	AL928690	Mouse DNA
15	20	4.0	103244	3	AC090524	Caenorhab
16	20	4.0	154174	5	AL935289	Zebrafish
17	20	4.0	169258	10	AC132324	Mus muscu
18	20	4.0	171813	2	AC022722	Homo sapi
19	20	4.0	172801	2	AC110908	Mus muscu
20	20	4.0	174632	2	BX897657	Danio rer
21	20	4.0	179071	2	AC146665	Homo sapi
C 22	20	4.0	180035	2	AC142504	Human chr
C 23	20	4.0	181833	9	CNS05TEN	Mus muscu
24	20	4.0	187487	2	AC147509	Mus muscu
25	20	4.0	193781	2	AC138282	Mus muscu
26	20	4.0	194596	2	AC140365	Mus muscu
27	20	4.0	195897	2	AC123873	Mus muscu
28	20	4.0	203526	2	AC124606	Mus muscu
29	20	4.0	208587	10	AC124599	Mus muscu
30	20	4.0	211189	2	AC140234	Mus muscu
31	20	4.0	211584	2	AC141645	Mus muscu
32	20	4.0	214574	2	AC124589	Mus muscu
C 33	20	4.0	216667	10	AC125326	Mus muscu
C 34	20	4.0	216911	2	AC126035	Mus muscu
C 35	20	4.0	217825	10	AC132950	Mus muscu
C 36	20	4.0	249688	2	AC126446	Mus muscu
C 37	20	4.0	257013	10	AC114915	Mus muscu
C 38	20	4.0	261333	2	AC138280	Mus muscu
C 39	20	4.0	287664	2	AC109210	Mus muscu
C 40	20	4.0	346516	2	AC138181	Mus muscu
C 41	19	3.8	628	11	HS369F10	STS from
C 42	19	3.8	725	11	BV056433	S212P6531
C 43	19	3.8	852	6	BD186721	Nucleic a
C 44	19	3.8	1024	5	AF217081	Takydromu
C 45	19	3.8	1225	3	AF200389	Ceratosol
46	19	3.8	1829	3	AF200387	Ceratosol
C 47	19	3.8	2027	9	AB051154	Macaca fa
C 48	19	3.8	6971	6	AX344652	Sequence
C 49	19	3.8	7501	1	AE002162	Chlamydia
50	19	3.8	7502	1	CTPLORF	Chlamydia m
C 51	19	3.8	15373	6	AX345369	Sequence
52	19	3.8	22690	1	AB030032	Actinobac
53	19	3.8	23112	1	AB010415	Actinobac
C 54	19	3.8	27210	9	HS422E10	Human DNA
55	19	3.8	34372	3	US8727	Caenorhabdi
56	19	3.8	37282	3	CEF38A1	Caenorhabdi
57	19	3.8	44237	3	CER05H10	Caenorhabdi
58	19	3.8	50793	2	AC129176	Mus muscu
59	19	3.8	55299	3	AC024830	Caenorhab
C 60	19	3.8	72421	2	AC101509	Mus muscu
C 61	19	3.8	86428	2	AC126016	Medicago
C 62	19	3.8	93407	9	AC011383	Homo sapi
C 63	19	3.8	104186	5	BX088536	Zebrafish
64	19	3.8	107733	9	AC008472	Homo sapi
C 65	19	3.8	110000	3	AC116984_3	Continuation (4 of

C 66	19	3.8	110602	2	AL358592	Homo sapi	139	18	3.6	1923	14	AB064414	AB064414 Influenza
C 67	19	3.8	114501	2	AP005093	Oryza sat	140	18	3.6	1961	14	D78433	D78433 Influenza C
C 68	19	3.8	118955	9	AC068274	Homo sapi	C 141	18	3.6	2000	6	AX655128	AX655128 Sequence C
C 69	19	3.8	122051	2	AC146664	Medicago	C 142	18	3.6	2010	14	FLCHAM	FLCHAM Influenza C
C 70	19	3.8	122051	2	AC146664	Medicago	C 143	18	3.6	2706	6	AX086825	AX086825 Sequence
C 71	19	3.8	133860	2	AL157709	Human DNA	C 144	18	3.6	2706	6	AX086825	AX086825 Sequence
C 72	19	3.8	133860	2	AL157709	Human DNA	C 145	18	3.6	2713	6	AX057287	AX057287 Homo sapi
C 73	19	3.8	137525	8	AP005397	Oryza sat	C 146	18	3.6	2713	6	AX057287	AX057287 Homo sapi
C 74	19	3.8	139035	9	AL356102	Human DNA	C 147	18	3.6	2797	9	BC060798	BC060798 Homo sapi
C 75	19	3.8	142123	9	AC004690	Homo sapi	C 148	18	3.6	2797	9	BC060798	BC060798 Homo sapi
C 76	19	3.8	143968	2	AC116117	Mus muscu	C 149	18	3.6	3257	3	AF056111	AF056111 Globodera
C 77	19	3.8	143968	2	AC116117	Mus muscu	C 150	18	3.6	3257	3	AF056111	AF056111 Globodera
C 78	19	3.8	149933	9	HSBA3735	Human DNA	C 151	18	3.6	3293	3	AF069242	AF069242 Homo sapi
C 79	19	3.8	150312	9	CNS01RIU	Human DNA	C 152	18	3.6	3293	3	AF069242	AF069242 Homo sapi
C 80	19	3.8	151171	2	AC020775	Homo sapi	C 153	18	3.6	3373	9	HSBA3735	HSBA3735 Sequence
C 81	19	3.8	156820	2	AC136266	Rattus no	C 154	18	3.6	3373	9	HSBA3735	HSBA3735 Sequence
C 82	19	3.8	157545	2	AL163535	Homo sapi	C 155	18	3.6	4025	10	AF132672	AF132672 Rattus no
C 83	19	3.8	161871	2	AC136912	Homo sapi	C 156	18	3.6	4025	10	AF132672	AF132672 Rattus no
C 84	19	3.8	162342	9	AC009041	Mus muscu	C 157	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 85	19	3.8	162342	9	AC009041	Mus muscu	C 158	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 86	19	3.8	162342	9	AC009041	Mus muscu	C 159	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 87	19	3.8	162342	9	AC009041	Mus muscu	C 160	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 88	19	3.8	167424	2	AC111075	Mus muscu	C 161	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 89	19	3.8	167424	2	AC111075	Mus muscu	C 162	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 90	19	3.8	167424	2	AC111075	Mus muscu	C 163	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 91	19	3.8	167424	2	AC111075	Mus muscu	C 164	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 92	19	3.8	167424	2	AC111075	Mus muscu	C 165	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 93	19	3.8	167424	2	AC111075	Mus muscu	C 166	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 94	19	3.8	167424	2	AC111075	Mus muscu	C 167	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 95	19	3.8	167424	2	AC111075	Mus muscu	C 168	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 96	19	3.8	167424	2	AC111075	Mus muscu	C 169	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 97	19	3.8	167424	2	AC111075	Mus muscu	C 170	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 98	19	3.8	167424	2	AC111075	Mus muscu	C 171	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 99	19	3.8	167424	2	AC111075	Mus muscu	C 172	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 100	19	3.8	167424	2	AC111075	Mus muscu	C 173	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 101	19	3.8	167424	2	AC111075	Mus muscu	C 174	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 102	19	3.8	167424	2	AC111075	Mus muscu	C 175	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 103	19	3.8	167424	2	AC111075	Mus muscu	C 176	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 104	19	3.8	167424	2	AC111075	Mus muscu	C 177	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 105	19	3.8	167424	2	AC111075	Mus muscu	C 178	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 106	19	3.8	167424	2	AC111075	Mus muscu	C 179	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 107	19	3.8	167424	2	AC111075	Mus muscu	C 180	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 108	19	3.8	167424	2	AC111075	Mus muscu	C 181	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 109	19	3.8	167424	2	AC111075	Mus muscu	C 182	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 110	19	3.8	167424	2	AC111075	Mus muscu	C 183	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 111	19	3.8	167424	2	AC111075	Mus muscu	C 184	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 112	19	3.8	167424	2	AC111075	Mus muscu	C 185	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
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C 114	19	3.8	167424	2	AC111075	Mus muscu	C 187	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
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C 117	19	3.8	167424	2	AC111075	Mus muscu	C 190	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 118	19	3.8	167424	2	AC111075	Mus muscu	C 191	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 119	19	3.8	167424	2	AC111075	Mus muscu	C 192	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 120	19	3.8	167424	2	AC111075	Mus muscu	C 193	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 121	19	3.8	167424	2	AC111075	Mus muscu	C 194	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 122	19	3.8	167424	2	AC111075	Mus muscu	C 195	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 123	19	3.8	167424	2	AC111075	Mus muscu	C 196	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 124	19	3.8	167424	2	AC111075	Mus muscu	C 197	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 125	19	3.8	167424	2	AC111075	Mus muscu	C 198	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 126	19	3.8	167424	2	AC111075	Mus muscu	C 199	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 127	19	3.8	167424	2	AC111075	Mus muscu	C 200	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 128	19	3.8	167424	2	AC111075	Mus muscu	C 201	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 129	19	3.8	167424	2	AC111075	Mus muscu	C 202	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 130	19	3.8	167424	2	AC111075	Mus muscu	C 203	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 131	19	3.8	167424	2	AC111075	Mus muscu	C 204	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 132	19	3.8	167424	2	AC111075	Mus muscu	C 205	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 133	19	3.8	167424	2	AC111075	Mus muscu	C 206	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 134	19	3.8	167424	2	AC111075	Mus muscu	C 207	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 135	19	3.8	167424	2	AC111075	Mus muscu	C 208	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 136	19	3.8	167424	2	AC111075	Mus muscu	C 209	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 137	19	3.8	167424	2	AC111075	Mus muscu	C 210	18	3.6	4131	3	AGA535206	AGA535206 Anopheles
C 138	19	3.8	167424	2	AC111075	Mus muscu	C 211	18	3.6	4131	3	AGA535206	AGA535206 Anopheles

358	18	3..6	270169	2	AC103230	AC103230 Rattus no	431	17	3..4	10233	1	AE011023	AE011023 Methanosa
359	18	3..6	272329	2	AC094789	AC094789 Rattus no	432	17	3..4	10356	9	AC093380	AC093380 Homo sapi
360	18	3..6	272329	2	AC094789	AC094789 Rattus no	433	17	3..4	10661	1	AE006119	AE006119 Pasteurel
361	18	3..6	273105	2	AC112439	AC112439 Rattus no	434	17	3..4	10757	1	AE008389	AE008389 Streptoco
362	18	3..6	276719	2	AC111548	AC111548 Rattus no	435	17	3..4	10882	1	AE007322	AE007322 Streptoco
363	18	3..6	298700	1	AP005951	AP005951 Bradyrhiz	436	17	3..4	11032	1	AE013267	AE013267 Methanosa
364	18	3..6	299903	3	AE003514	AE003514 Drosophill	437	17	3..4	11296	1	AE010130	AE010130 Archaeogl
365	18	3..6	300217	1	AE016922	AE016922 Chromobac	438	17	3..4	11301	1	AE007492	AE007492 Streptoco
366	18	3..6	300511	1	AE016775	AE016775 Pseudomon	439	17	3..4	11443	6	AR218817	AR218817 Sequence
367	18	3..6	301439	1	AE015943	AE015943 Clostridi	440	17	3..4	11443	6	BD003729	BD003729 Polynucle
368	18	3..6	301838	1	AE017209	AE017209 Geobacter	441	17	3..4	11937	1	AE012277	AE012277 Xanthomon
369	18	3..6	308435	2	AC099254	AC099254 Rattus no	442	17	3..4	12503	8	CLZMRPB	CLZMRPB
370	18	3..6	314306	3	AE003594	AE003594 Drosophill	443	17	3..4	12855	1	AE007455	AE007455 Streptoco
371	18	3..6	315752	2	AC120285	AC120285 Rattus no	444	17	3..4	14277	3	CEY44A6B	CEY44A6B
372	18	3..6	315844	3	AE003671	AE003671 Drosophill	445	17	3..4	14619	3	CFP58D12	CFP58D12
373	18	3..6	324688	2	AC111620	AC111620 Rattus no	446	17	3..4	17913	10	WU0278574	WU0278574
374	18	3..6	325265	2	AC111802	AC111802 Rattus no	447	17	3..4	18420	2	AC017154	AC017154 Drosophill
375	18	3..6	349742	1	BX572090	BX572090 Prochloro	448	17	3..4	19292	3	CEY76A2A	CEY76A2A
376	18	3..6	349980	6	AX344573	AX344573 Sequence	449	17	3..4	20539	9	HS349E10	HS349E10
377	17	3..4	558	11	G94778	G94778 S208P6807RE	450	17	3..4	21245	8	AB027572	AB027572 Triticum
378	17	3..4	645	6	BD064358	BD064358 Novel cod	451	17	3..4	22724	10	BX470094	BX470094 Mouse DNA
379	17	3..4	648	11	BV056832	BV056832 S212P6827	452	17	3..4	24711	3	AF039036	AF039036 Caenorhab
380	17	3..4	696	6	AX194063	AX194063 Sequence	453	17	3..4	25245	3	AF040644	AF040644 Caenorhab
381	17	3..4	720	6	AX194289	AX194289 Sequence	454	17	3..4	25750	3	AF016413	AF016413 Caenorhab
382	17	3..4	744	6	AX570108	AX570108 Sequence	455	17	3..4	25777	3	AC024828	AC024828 Caenorhab
383	17	3..4	764	11	BV024119	BV024119 S212P6031	456	17	3..4	28466	3	U88171	U88171 Caenorhabdi
384	17	3..4	965	6	AX753003	AX753003 Sequence	457	17	3..4	28473	6	AR218851	AR218851 Sequence
385	17	3..4	969	1	AF485768	AF485768 Aeromonas	458	17	3..4	28473	6	BD003763	BD003763 Polynucle
386	17	3..4	1013	9	HSEKNE	X00187 Human prepr	459	17	3..4	29145	10	AF127669	AF127669 Mus muscu
387	17	3..4	1203	9	F202550S15	AF202564 Homo sapi	460	17	3..4	29257	9	AL596115	AL596115 Human DNA
388	17	3..4	1219	10	MDL132555	ADJ132555 Mus platy	461	17	3..4	29370	3	U58760	U58760 Caenorhabdi
389	17	3..4	1243	6	BD190961	BD190961 DNA methy	462	17	3..4	29442	9	AL355855	AL355855 Human DNA
390	17	3..4	1329	1	STRPURI5YN	LI5190 Streptococc	463	17	3..4	30355	2	AL358948	AL358948 Homo sapi
391	17	3..4	1629	6	AX764604	AX764604 Sequence	464	17	3..4	30522	3	U70853	U70853 Caenorhabdi
392	17	3..4	1703	10	BC029630	BC029630 Mus muscu	465	17	3..4	30836	3	U67948	U67948 Caenorhabdi
393	17	3..4	1768	9	D50001S01	D50001 Homo sapien	466	17	3..4	30973	3	AC006644	AC006644 Caenorhab
394	17	3..4	1813	6	AR379862	AR379862 Sequence	467	17	3..4	31678	3	CET05A1	CET05A1
395	17	3..4	2106	8	AF013693	AF013693 Codonanth	468	17	3..4	32063	3	CECC4	CECC4
396	17	3..4	2119	3	AF159419	AF159419 Drosophill	469	17	3..4	32377	3	CFT08G5	CFT08G5
397	17	3..4	2414	6	AX878253	AX878253 Sequence	470	17	3..4	32635	2	AC095863	AC095863
398	17	3..4	2414	6	BD157110	BD157110 Primer fo	471	17	3..4	33359	3	CFP55B11	CFP55B11
399	17	3..4	2414	9	AK002141	AK002141 Homo sapi	472	17	3..4	34162	9	HSU139A4	HSU139A4
400	17	3..4	2528	1	AEOCYTENT	M84709 Aeromonas h	473	17	3..4	34497	3	U43282	U43282 Caenorhabdi
401	17	3..4	2546	6	A94935	A94935 Sequence 20	474	17	3..4	34759	3	CEC34C12	CEC34C12
402	17	3..4	2763	5	CHKPECM	BC040316 Homo sapi	475	17	3..4	35018	3	CEC34C12	CEC34C12
403	17	3..4	2872	9	BC040316	BC040316 Homo sapi	476	17	3..4	35962	6	AX598904	AX598904 Sequence
404	17	3..4	2877	6	BD227594	BD227594 C. albica	477	17	3..4	36250	9	AC138372	AC138372 Homo sapi
405	17	3..4	2877	6	AC023760	AC023760 Sequence	478	17	3..4	36516	10	AF387339	AF387339 Rattus no
406	17	3..4	3109	6	AX833797	AX833797 Sequence	479	17	3..4	38261	3	U23171	U23171 Caenorhabdi
407	17	3..4	3109	9	AK095811	AK095811 Homo sapi	480	17	3..4	38702	3	AC006646	AC006646 Caenorhab
408	17	3..4	3272	8	AK110021	AK110021 Oryza sat	481	17	3..4	39750	3	CBC41C4	CBC41C4
409	17	3..4	3666	3	AX155564	AX155564 Ochlerota	482	17	3..4	41247	9	HSU220B11	HSU220B11
410	17	3..4	3672	8	ACH132014	AJ132014 Acremoniu	483	17	3..4	41305	3	CFP58D5	CFP58D5
411	17	3..4	3726	6	AX571586	AX571586 Sequence	484	17	3..4	41818	2	AC018239	AC018239 Drosophill
412	17	3..4	3925	9	AK124692	AK124692 Homo sapi	485	17	3..4	41859	2	AC145437	AC145437 Oryza sat
413	17	3..4	3978	2	AK017659	AK017659 Drosophill	486	17	3..4	42551	2	AC142470	AC142470 Homo sapi
414	17	3..4	4565	8	D78336	D78336 Oryza sativ	487	17	3..4	42854	8	SPAC17A5	SPAC17A5
415	17	3..4	4852	1	P025130	U25130 Pseudomonas	488	17	3..4	42981	3	AF025472	AF025472 Caenorhab
416	17	3..4	4871	9	HSA278993	AJ278993 Homo sapi	489	17	3..4	43262	9	AL137014	AL137014 Human DNA
417	17	3..4	4940	9	AF180682	AF180682 Homo sapi	490	17	3..4	43809	3	AC006618	AC006618 Caenorhab
418	17	3..4	5165	3	DROCOPIA	D10880 Drosophilla	491	17	3..4	44171	3	AF000265	AF000265 Caenorhab
419	17	3..4	5434	6	AX330730	AX330730 Sequence	492	17	3..4	44226	2	AC142400	AC142400 Homo sapi
420	17	3..4	5434	6	AX330939	AX330939 Sequence	493	17	3..4	44621	9	AF001873	AF001873 Homo sapi
421	17	3..4	5434	6	AX332235	AX332235 Sequence	494	17	3..4	46255	3	U20861	U20861 Caenorhabdi
422	17	3..4	5434	9	HSDNMTASE	X63692 H.sapiens m	495	17	3..4	46934	9	AC010077	AC010077 Homo sapi
423	17	3..4	5455	5	U00455	U00455 Acipenser t	496	17	3..4	47226	2	AC105215	AC105215 Homo sapi
424	17	3..4	5771	6	AX346853	AX346853 Sequence	497	17	3..4	48460	2	AC101029	AC101029 Mus muscu
425	17	3..4	6069	9	HSU42391	U42391 Human myosi	498	17	3..4	48797	9	AC103582	AC103582 Homo sapi
426	17	3..4	8471	1	STRCONAA	M36180 Streptococc	499	17	3..4	53390	2	CEH16F20	CEH16F20
427	17	3..4	8028	8	TOMFSPG	M87659 Tomato frui	500	17	3..4	54797	2	SPNEU1920	SPNEU1920
428	17	3..4	9905	6	AX344964	AX344964 Sequence	501	17	3..4	55480	9	AL358933	AL358933 Human DNA
429	17	3..4	9975	1	AE001048	AE001048 Archaeogl	502	17	3..4	56173	9	AC011390	AC011390 Homo sapi
430	17	3..4	10029	1	AE008548	AE008548 Streptoco	503	17	3..4	58947	3	AC024869	AC024869 Caenorhab

504	17	3.4	59228	2	AC069452	AC069452 Homo sapi	577	17	3.4	110000	2	BX323988_0	BX323988_0
505	17	3.4	59533	3	AC084450	AC084450 Caenorhab	c 578	17	3.4	110000	2	CEX10588_3	CEX10588_3
506	17	3.4	61017	2	AC099990	Mus muscu	c 579	17	3.4	110000	2	CEX11182_2	CEX11182_2
507	17	3.4	61448	2	AC100679	Mus muscu	c 580	17	3.4	110000	6	AR406002_1	AR406002_1
508	17	3.4	63949	9	AC005903	Homo sapi	c 581	17	3.4	110000	8	AC145127_17	AC145127_17
509	17	3.4	64258	8	BX842595	Neurospor	c 582	17	3.4	110000	8	AC145127_18	AC145127_18
510	17	3.4	64667	10	BX000436	Mouse DNA	c 583	17	3.4	110000	10	AE014176_2	AE014176_2
511	17	3.4	69308	2	AC101539	Mus muscu	c 584	17	3.4	110000	2	AL451162	AL451162
512	17	3.4	69577	2	AC014098	Drosophil	c 585	17	3.4	113477	2	AC009458	AC009458
513	17	3.4	69814	2	AC129565	Mus muscu	c 586	17	3.4	113098	2	AC009458	AC009458
514	17	3.4	70694	3	AC006708	Caenorhab	c 587	17	3.4	113250	9	AC004900	AC004900
515	17	3.4	73145	2	AC009767	Homo sapi	c 588	17	3.4	116821	9	AL606537	AL606537
516	17	3.4	73169	2	AC100699	Mus muscu	c 589	17	3.4	117026	9	HS329A5	HS329A5
517	17	3.4	73233	2	AC116222	Rattus no	c 590	17	3.4	117751	9	AC020913	AC020913
518	17	3.4	73233	2	AC024421	Homo sapi	c 591	17	3.4	118405	9	AC012349	AC012349
519	17	3.4	75125	8	AB025604	Arabidops	c 592	17	3.4	119008	9	HS111J24	HS111J24
520	17	3.4	77422	3	AC025723	Caenorhab	c 593	17	3.4	120027	2	AC020981	AC020981
521	17	3.4	77439	9	HS127F18	Human DNA	c 594	17	3.4	121143	8	AC144484	AC144484
522	17	3.4	77673	2	AC120790	Mus muscu	c 595	17	3.4	121609	2	AC137653	AC137653
523	17	3.4	78153	3	CEY53C10A	AL033536 Caenorhab	c 596	17	3.4	121902	9	AC008386	AC008386
524	17	3.4	78449	2	AC141965	AL033536 Caenorhab	c 597	17	3.4	122916	9	AL162716	AL162716
525	17	3.4	81207	9	HS125I3	AL033536 Caenorhab	c 598	17	3.4	124836	9	AC003085	AC003085
526	17	3.4	81250	9	AC124298	Human DNA	c 599	17	3.4	125590	3	CEY49E10	CEY49E10
527	17	3.4	81299	9	AL140044	Mus muscu	c 600	17	3.4	125798	9	AL390248	AL390248
528	17	3.4	84615	9	AL354747	Human DNA	c 601	17	3.4	125936	8	AC122148	AC122148
529	17	3.4	85644	3	AC084463	AL033536 Caenorhab	c 602	17	3.4	126708	8	AC118340	AC118340
530	17	3.4	86052	2	AC015946	Mus muscu	c 603	17	3.4	127091	2	AC009843	AC009843
531	17	3.4	86141	9	BX323845	Human DNA	c 604	17	3.4	128235	9	HSJ955C14	HSJ955C14
532	17	3.4	87635	10	AL929052	AL929052 Mouse DNA	c 605	17	3.4	128747	10	AL669846	AL669846
533	17	3.4	88382	2	AC018394	Homo sapi	c 606	17	3.4	128765	9	AL355852	AL355852
534	17	3.4	88955	9	AY442342	Homo sapi	c 607	17	3.4	129318	8	AC121233	AC121233
535	17	3.4	89350	8	ATT12H17	AL021635 Arabidops	c 608	17	3.4	129503	2	AC044863	AC044863
536	17	3.4	89370	3	AC084153	AL021635 Arabidops	c 609	17	3.4	129987	10	AL669940	AL669940
537	17	3.4	89728	9	AL583805	AL583805 Human DNA	c 610	17	3.4	130656	8	AL145491	AL145491
538	17	3.4	90526	9	AC092393	AL583805 Human DNA	c 611	17	3.4	130785	2	AC145414	AC145414
539	17	3.4	91814	3	AL513547	AL513547 Human DNA	c 612	17	3.4	131616	10	AL840632	AL840632
540	17	3.4	91820	3	AC084161	AL513547 Human DNA	c 613	17	3.4	131704	2	AP004313	AP004313
541	17	3.4	92613	2	AC081839	AL011839 Homo sapi	c 614	17	3.4	131998	9	HSJ277546	HSJ277546
542	17	3.4	93959	9	HS106C24	Z83313 Human DNA	c 615	17	3.4	132003	9	AC024351	AC024351
543	17	3.4	94734	9	HS232P20	AL021328 Human DNA	c 616	17	3.4	132010	2	AC073332	AC073332
544	17	3.4	94770	9	HSJ657D12	AL010943 Human DNA	c 617	17	3.4	132131	2	AC073332	AC073332
545	17	3.4	95449	9	AP001620	AP001620 Homo sapi	c 618	17	3.4	132396	2	BX571845	BX571845
546	17	3.4	96595	6	AX695617	AX695617 Sequence	c 619	17	3.4	132508	8	AC141323	AC141323
547	17	3.4	96642	9	AC002291	AC002291 Arabidops	c 620	17	3.4	132749	2	AC006778	AC006778
548	17	3.4	97711	8	ATT16K5	AL132965 Arabidops	c 621	17	3.4	133028	8	AC134967	AC134967
549	17	3.4	97995	9	AC067718	AL067718 Homo sapi	c 622	17	3.4	133052	9	AL136325	AL136325
550	17	3.4	99897	9	AC093584	AC093584 Homo sapi	c 623	17	3.4	133121	8	AC092553	AC092553
551	17	3.4	100369	9	AL139258	AL139258 Human DNA	c 624	17	3.4	133705	2	AC137618	AC137618
552	17	3.4	101216	2	AC110722	AC110722 Danio rer	c 625	17	3.4	134273	8	AP005469	AP005469
553	17	3.4	101565	8	AC145753	AC145753 Genomic s	c 626	17	3.4	134525	8	CHOSXX	CHOSXX
554	17	3.4	102008	2	AC145753	AC145753 Homo sapi	c 627	17	3.4	134545	8	AB042240	AB042240
555	17	3.4	103040	9	AC104966	AC104966 Homo sapi	c 628	17	3.4	134867	2	AC013788	AC013788
556	17	3.4	103069	9	AL606469	AL606469 Human DNA	c 629	17	3.4	134933	8	AC092750	AC092750
557	17	3.4	105211	9	AC110076	AC110076 Homo sapi	c 630	17	3.4	134985	2	AC146941	AC146941
558	17	3.4	105392	9	AC073215	AC073215 Homo sapi	c 631	17	3.4	135050	2	AC118536	AC118536
559	17	3.4	105600	8	AP005173	AP005173 Oryza sat	c 632	17	3.4	135252	5	BX119965	BX119965
560	17	3.4	107044	9	AC011375	AC011375 Homo sapi	c 633	17	3.4	135273	5	AC084761	AC084761
561	17	3.4	107238	9	AC106786	AC106786 Homo sapi	c 634	17	3.4	135286	10	AL928905	AL928905
562	17	3.4	107714	2	AL356306	AL356306 Homo sapi	c 635	17	3.4	135619	9	AL354809	AL354809
563	17	3.4	108158	8	ATF3A4	AL132978 Arabidops	c 636	17	3.4	136002	9	AL450426	AL450426
564	17	3.4	109148	2	AC138439	AC138439 Takifugu	c 637	17	3.4	136228	2	AC067916	AC067916
565	17	3.4	110000	2	AC095863	Continuation (3 of	c 638	17	3.4	136787	2	AC132483	AC132483
566	17	3.4	110000	2	AC095863	Continuation (3 of	c 639	17	3.4	137259	2	AC010392	AC010392
567	17	3.4	110000	2	AC116222	Continuation (3 of	c 640	17	3.4	137515	2	DMBR12B22	DMBR12B22
568	17	3.4	110000	2	AC112804	AC112804 Rattus no	c 641	17	3.4	137724	8	AC004884	AC004884
569	17	3.4	110000	2	AC118330	Continuation (3 of	c 642	17	3.4	138244	9	AC004884	AC004884
570	17	3.4	110000	2	AC120922	Continuation (3 of	c 643	17	3.4	138981	9	AC141002	AC141002
571	17	3.4	110000	2	AC120932	AC120932 Rattus no	c 644	17	3.4	139111	9	AL158048	AL158048
572	17	3.4	110000	2	AC139489	AC139489 Homo sapi	c 645	17	3.4	139166	9	AC011750	AC011750
573	17	3.4	110000	2	AC139489	Continuation (2 of	c 646	17	3.4	139712	2	AC145828	AC145828
574	17	3.4	110000	2	AC140148	Continuation (3 of	c 647	17	3.4	139752	2	AC136521	AC136521
575	17	3.4	110000	2	AC142490	AC142490 Mus muscu	c 648	17	3.4	139873	9	AC010612	AC010612
576	17	3.4	110000	2	AC146445	Continuation (2 of	c 649	17	3.4	140384	8	ZMA86563	ZMA86563

c 650	17	3.4	140403	2	AC109444	AC109444 Homo sapi	723	17	3.4	154888	2	BX97659	BX97659 Danio rer
651	17	3.4	140763	2	AC144549	AC144549 Sorghum b	c 724	17	3.4	154931	2	BX649585	BX649585 Danio rer
652	17	3.4	140854	9	AC108038	Homo sapi	c 725	17	3.4	154995	2	AC011979	AC011979 Homo sapi
c 653	17	3.4	141432	2	AC015699	AC015699 Homo sapi	c 726	17	3.4	155334	2	AC011156	AC011156 Homo sapi
c 654	17	3.4	141899	2	AC087457	AC087457 Homo sapi	c 727	17	3.4	155411	10	AC133602	AC133602 Mus muscu
c 655	17	3.4	141925	2	AC098702	AC098702 Felis cat	c 728	17	3.4	155510	2	AL353723	AL353723 Homo sapi
656	17	3.4	142420	8	AL138816	AL138816 Human DNA	729	17	3.4	155612	3	AC091228	AC091228 Drosophil
657	17	3.4	142510	8	AP005813	AP005813 Oryza sat	730	17	3.4	156249	2	BX276184	BX276184 Danio rer
c 658	17	3.4	142638	9	AL355316	AL355316 Human DNA	c 731	17	3.4	156249	2	BX276184	BX276184 Danio rer
c 659	17	3.4	142641	9	AC132068	AC132068 Homo sapi	c 732	17	3.4	156441	9	AC091869	AC091869 Homo sapi
c 660	17	3.4	143065	2	AC105375	AC105375 Felis cat	733	17	3.4	156677	2	AC092550	AC092550 Homo sapi
c 661	17	3.4	143283	9	AC016763	AC016763 Homo sapi	734	17	3.4	156955	2	AP001908	AP001908 Homo sapi
662	17	3.4	143487	2	AC141129	AC141129 Rattus no	735	17	3.4	157080	2	AL358856	AL358856 Homo sapi
663	17	3.4	143798	9	AL157409	AL157409 Human DNA	736	17	3.4	157390	2	BX324227	BX324227 Danio rer
c 664	17	3.4	143878	9	AC003074	AC003074 Homo sapi	737	17	3.4	157722	10	AL953890	AL953890 Mouse DNA
665	17	3.4	143893	2	AC010766	AC010766 Homo sapi	738	17	3.4	157788	2	AV178786	AV178786 Canis fam
666	17	3.4	144410	2	AC120841	AC120841 Mus muscu	c 739	17	3.4	157792	9	AC069209	AC069209 Homo sapi
c 667	17	3.4	144734	2	AP001839	AP001839 Homo sapi	c 740	17	3.4	157833	9	AC132186	AC132186 Homo sapi
668	17	3.4	145980	8	OSN000291	OSN000291	c 741	17	3.4	157891	10	AC133161	AC133161 Mus muscu
c 669	17	3.4	146083	8	AP003315	AP003315 Oryza sat	c 742	17	3.4	158027	10	AC125093	AC125093 Mus muscu
c 670	17	3.4	146099	2	AC011192	AC011192 Homo sapi	743	17	3.4	158034	2	AC019275	AC019275 Homo sapi
c 671	17	3.4	146112	9	HS592A1	HS592A1 Human DNA	c 744	17	3.4	158091	9	AC140171	AC140171 Homo sapi
672	17	3.4	146144	8	AP003331	AP003331 Oryza sat	c 745	17	3.4	158264	2	AC015497	AC015497 Homo sapi
673	17	3.4	146275	2	AC080119	AC080119 Homo sapi	746	17	3.4	158312	2	AC083922	AC083922 Homo sapi
674	17	3.4	146464	5	BX530024	BX530024 Zebraphish	747	17	3.4	158401	2	AC068521	AC068521 Homo sapi
c 675	17	3.4	146699	9	BS000226	BS000226 Pan trogl	c 748	17	3.4	158544	2	AC023658	AC023658 Homo sapi
c 676	17	3.4	146708	2	BX321881	BX321881 Mus muscu	c 749	17	3.4	158736	2	AC011019	AC011019 Homo sapi
c 677	17	3.4	146961	2	AL355525	AL355525 Homo sapi	750	17	3.4	158966	2	AC113296	AC113296 Mus muscu
678	17	3.4	147207	2	AC078890	AC078890 Oryza sat	c 751	17	3.4	158983	3	AC005374	AC005374 Drosophil
c 679	17	3.4	147310	2	AL513495	AL513495 Homo sapi	752	17	3.4	159150	2	AC104279	AC104279 Oryza sat
c 680	17	3.4	147500	8	AP004849	AP004849 Oryza sat	753	17	3.4	159300	9	HS279F22	HS279F22 Homo sapi
c 681	17	3.4	147663	2	AC118259	AC118259 Mus muscu	c 754	17	3.4	159312	2	AC096878	AC096878 Pan trogl
c 682	17	3.4	147728	2	AC034113	AC034113 Homo sapi	755	17	3.4	159438	2	AC016621	AC016621 Homo sapi
c 683	17	3.4	148115	2	AC125498	AC125498 Danio rer	c 756	17	3.4	159445	9	AC092994	AC092994 Homo sapi
c 684	17	3.4	148248	2	RN235J17	RN235J17 Rattus no	c 757	17	3.4	159656	5	AL929243	AL929243 Zebraphish
685	17	3.4	148347	8	AP005408	AP005408 Oryza sat	c 758	17	3.4	159676	2	AC145239	AC145239 Mus muscu
c 686	17	3.4	148347	8	AP005408	AP005408 Oryza sat	c 759	17	3.4	159784	2	AC061996	AC061996 Homo sapi
c 687	17	3.4	148704	8	AC124213	AC124213 Genomic s	760	17	3.4	160096	2	AC022657	AC022657 Homo sapi
c 688	17	3.4	149338	2	AC129836	AC129836 Felis cat	c 761	17	3.4	160145	9	AL161612	AL161612 Human DNA
c 689	17	3.4	149618	9	AP000556	AP000556 Homo sapi	c 762	17	3.4	160283	9	AC011773	AC011773 Homo sapi
690	17	3.4	149622	2	AC074082	AC074082 Homo sapi	c 763	17	3.4	160370	9	AC023464	AC023464 Homo sapi
c 691	17	3.4	149910	9	AC023391	AC023391 Homo sapi	764	17	3.4	160943	9	AC074029	AC074029 Homo sapi
c 692	17	3.4	150036	9	AP000557	AP000557 Homo sapi	c 765	17	3.4	161103	9	AL392163	AL392163 Human DNA
693	17	3.4	150728	9	AC084277	AC084277 Homo sapi	766	17	3.4	161180	2	AC146771	AC146771 Canis fam
c 694	17	3.4	150728	9	AC084277	AC084277 Homo sapi	767	17	3.4	161306	2	AC091056	AC091056 Homo sapi
695	17	3.4	150728	8	AP003323	AP003323 Oryza sat	768	17	3.4	161348	10	AL645532	AL645532 Mouse DNA
c 696	17	3.4	151142	9	AC069275	AC069275 Homo sapi	769	17	3.4	161366	9	AC090939	AC090939 Homo sapi
c 697	17	3.4	151143	9	AC108714	AC108714 Homo sapi	c 770	17	3.4	161942	2	BX322538	BX322538 Danio rer
c 698	17	3.4	151173	8	AC135257	AC135257 Genomic s	771	17	3.4	162023	9	AC084033	AC084033 Homo sapi
c 699	17	3.4	151242	2	AC144589	AC144589 Homo sapi	772	17	3.4	162100	9	AC018868	AC018868 Homo sapi
700	17	3.4	151267	8	AC134932	AC134932 Oryza sat	773	17	3.4	162209	9	CNS01R1H	AL163195 Human chr
c 701	17	3.4	151733	2	AC079643	AC079643 Mus muscu	774	17	3.4	162457	2	BX000523	BX000523 Danio rer
c 702	17	3.4	151753	2	AC119614	AC119614 Rattus no	775	17	3.4	162564	10	AC127575	AC127575 Mus muscu
703	17	3.4	151973	2	OSN00178	OSN00178	c 776	17	3.4	162689	9	AC093657	AC093657 Homo sapi
c 704	17	3.4	152058	4	AC091756	AC091756 Sus scrof	c 777	17	3.4	162714	2	AC027569	AC027569 Homo sapi
c 705	17	3.4	152123	2	AC046190	AC046190 Homo sapi	778	17	3.4	162727	9	HS46711	HS46711 Human DNA
c 706	17	3.4	152295	2	AC139615	AC139615 Rattus no	779	17	3.4	162778	2	AC009559	AC009559 Homo sapi
c 707	17	3.4	152519	2	AC108898	AC108898 Felis cat	780	17	3.4	162837	2	AC142143	AC142143 Medicago
708	17	3.4	152547	2	AC118934	AC118934 Mus muscu	781	17	3.4	162955	9	AC012527	AC012527 Homo sapi
709	17	3.4	152910	8	AP005537	AP005537 Oryza sat	c 782	17	3.4	162980	2	BX276119	BX276119 Danio rer
710	17	3.4	152941	8	AP003044	AP003044 Oryza sat	c 783	17	3.4	163042	9	AC016245	AC016245 Homo sapi
711	17	3.4	153356	2	AC004995	AC004995 Homo sapi	784	17	3.4	163083	9	AC103773	AC103773 Homo sapi
712	17	3.4	153553	9	AC008627	AC008627 Homo sapi	c 785	17	3.4	163115	9	AC105902	AC105902 Homo sapi
713	17	3.4	153569	5	BX649231	BX649231 Zebraphish	c 786	17	3.4	163404	2	AC009614	AC009614 Homo sapi
c 714	17	3.4	153569	5	BX649231	BX649231 Zebraphish	787	17	3.4	163451	2	AC069468	AC069468 Mus muscu
715	17	3.4	153954	2	AL354862	AL354862 Human DNA	c 788	17	3.4	163546	2	AC103547	AC103547 Rattus no
c 716	17	3.4	153998	2	AC133529	AC133529 Homo sapi	789	17	3.4	163627	2	AC135031	AC135031 Rattus no
c 717	17	3.4	153999	9	AC131213	AC131213 Homo sapi	c 790	17	3.4	163871	9	HS1158E12	AL031584 Human DNA
718	17	3.4	154202	10	AC121947	AC121947 Mus muscu	791	17	3.4	163878	10	AC134563	AC134563 Mus muscu
719	17	3.4	154468	2	AC018409	AC018409 Homo sapi	c 792	17	3.4	163908	9	AC007050	AC007050 Homo sapi
720	17	3.4	154605	2	AC046161	AC046161 Homo sapi	c 793	17	3.4	163942	2	AC113989	AC113989 Mus muscu
721	17	3.4	154732	9	AC011700	AC011700 Homo sapi	c 794	17	3.4	164084	2	AC026580	AC026580 Homo sapi
722	17	3.4	154883	9	AC068711	AC068711 Homo sapi	c 795	17	3.4	164232	2	AC010855	AC010855 Homo sapi

796	17	3.4	164632	2	AC118434	AC118434 Rattus no	869	17	3.4	175494	2	AC127242	Mus muscu
797	17	3.4	164636	2	AC117783	AC117783 Mus muscu	870	17	3.4	175562	2	AC108413	Mus muscu
798	17	3.4	164801	2	AC117783	AC117783 Mus muscu	871	17	3.4	175930	2	AC116500	Mus muscu
799	17	3.4	164911	8	BSX248237	BSX248237 Danio rer	872	17	3.4	176051	9	AC023490	Homo sapi
800	17	3.4	165244	2	AC145039	AC145039 Bos tauru	873	17	3.4	176550	9	AL356356	Human DNA
801	17	3.4	165244	2	AC145039	AC145039 Bos tauru	874	17	3.4	176550	9	AL356356	Human DNA
802	17	3.4	165283	2	AC145039	AC145039 Bos tauru	875	17	3.4	176672	2	AC118125	Rattus no
803	17	3.4	165339	2	AC145039	AC145039 Bos tauru	876	17	3.4	176749	2	AC096748	Homo sapi
804	17	3.4	165346	2	AC145039	AC145039 Bos tauru	877	17	3.4	176762	10	AC096748	Homo sapi
805	17	3.4	165861	2	AC106812	AC106812 Homo sapi	878	17	3.4	176843	2	AC026655	Mouse DNA
806	17	3.4	166107	2	AC024427	AC024427 Homo sapi	879	17	3.4	177231	9	AC134772	Homo sapi
807	17	3.4	166107	2	AC024427	AC024427 Homo sapi	880	17	3.4	177423	2	AC120036	Homo sapi
808	17	3.4	166470	9	AC092695	AC092695 Homo sapi	881	17	3.4	177604	2	AC013342	Homo sapi
809	17	3.4	166850	2	AC012222	AC012222 Homo sapi	882	17	3.4	177862	9	AC084782	Homo sapi
810	17	3.4	166885	9	AC091873	AC091873 Homo sapi	883	17	3.4	177864	9	AC024996	Homo sapi
811	17	3.4	166892	2	AC009969	AC009969 Homo sapi	884	17	3.4	177929	2	AC133936	Mus muscu
812	17	3.4	166896	2	AC136511	AC136511 Pan trogl	885	17	3.4	177976	2	AC090755	Homo sapi
813	17	3.4	166896	2	AC136511	AC136511 Pan trogl	886	17	3.4	178097	2	AC009178	Homo sapi
814	17	3.4	167122	9	AC142322	AC142322 Pan trogl	887	17	3.4	178097	2	AC009178	Homo sapi
815	17	3.4	167122	9	AC142322	AC142322 Pan trogl	888	17	3.4	178209	2	AC115939	Mus muscu
816	17	3.4	167139	9	AC087710	AC087710 Homo sapi	889	17	3.4	178316	2	AC012105	Homo sapi
817	17	3.4	167203	8	AP003264	AP003264 Oryza sat	890	17	3.4	178316	2	AC012105	Homo sapi
818	17	3.4	167417	9	AC011505	AC011505 Homo sapi	891	17	3.4	178553	2	AC006891	Caenorhab
819	17	3.4	167570	9	AC092668	AC092668 Homo sapi	892	17	3.4	178553	2	AC006891	Caenorhab
820	17	3.4	167796	9	AC0109819	AC0109819 Homo sapi	893	17	3.4	178564	2	AC112669	Mus muscu
821	17	3.4	168172	9	AC010528	AC010528 Homo sapi	894	17	3.4	178640	2	AC069170	Homo sapi
822	17	3.4	168172	9	AC010528	AC010528 Homo sapi	895	17	3.4	178640	2	AC069170	Homo sapi
823	17	3.4	168257	5	AL929184	AL929184 Zebrafish	896	17	3.4	179198	3	AL592183	Human DNA
824	17	3.4	168357	9	AC073137	AC073137 Homo sapi	897	17	3.4	179205	3	AC023720	Drosophil
825	17	3.4	168357	9	AC073137	AC073137 Homo sapi	898	17	3.4	179223	2	AC141463	Homo sapi
826	17	3.4	168690	2	AC099695	AC099695 Mus muscu	899	17	3.4	179223	2	AC141463	Homo sapi
827	17	3.4	168690	2	AC099695	AC099695 Mus muscu	900	17	3.4	179259	2	AC129289	Mus muscu
828	17	3.4	168730	10	AC121597	AC121597 Mus muscu	901	17	3.4	179259	2	AC129289	Mus muscu
829	17	3.4	168736	2	AC019042	AC019042 Homo sapi	902	17	3.4	179454	9	AC044873	Homo sapi
830	17	3.4	168736	2	AC019042	AC019042 Homo sapi	903	17	3.4	179454	9	AC044873	Homo sapi
831	17	3.4	168959	2	AC141841	AC141841 Apis mell	904	17	3.4	179482	9	AC108849	Mus muscu
832	17	3.4	168959	2	AC141841	AC141841 Apis mell	905	17	3.4	179482	9	AC108849	Mus muscu
833	17	3.4	169251	2	AC125006	AC125006 Mus muscu	906	17	3.4	179482	9	AC108849	Mus muscu
834	17	3.4	169251	2	AC125006	AC125006 Mus muscu	907	17	3.4	180141	9	AC023090	Homo sapi
835	17	3.4	169592	2	AC091674	AC091674 Homo sapi	908	17	3.4	180141	9	AC023090	Homo sapi
836	17	3.4	169592	2	AC091674	AC091674 Homo sapi	909	17	3.4	180366	5	EX000473	Zebrafish
837	17	3.4	169998	2	AC016578	AC016578 Homo sapi	910	17	3.4	180366	5	EX000473	Zebrafish
838	17	3.4	170071	2	AC084733	AC084733 Homo sapi	911	17	3.4	180460	9	CNS0518V	Human chr
839	17	3.4	170188	9	HS109F14	HS109F14 Human DNA	912	17	3.4	180460	9	CNS0518V	Human chr
840	17	3.4	170245	9	HS109F14	HS109F14 Human DNA	913	17	3.4	180460	9	CNS0518V	Human chr
841	17	3.4	170279	2	AC027053	AC027053 Homo sapi	914	17	3.4	180460	9	CNS0518V	Human chr
842	17	3.4	170334	9	AC016579	AC016579 Homo sapi	915	17	3.4	180460	9	CNS0518V	Human chr
843	17	3.4	170453	2	AC102335	AC102335 Mus muscu	916	17	3.4	180460	9	CNS0518V	Human chr
844	17	3.4	170966	2	AC121194	AC121194 Rattus no	917	17	3.4	180460	9	CNS0518V	Human chr
845	17	3.4	171104	2	EX649545	EX649545 Danio rer	918	17	3.4	180460	9	CNS0518V	Human chr
846	17	3.4	171170	2	AC146337	AC146337 Pan trogl	919	17	3.4	180460	9	CNS0518V	Human chr
847	17	3.4	171298	2	EX677674	EX677674 Mus muscu	920	17	3.4	180460	9	CNS0518V	Human chr
848	17	3.4	171705	2	AC027015	AC027015 Homo sapi	921	17	3.4	180460	9	CNS0518V	Human chr
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850	17	3.4	171905	2	AL591609	AL591609 Homo sapi	923	17	3.4	180460	9	CNS0518V	Human chr
851	17	3.4	172087	2	EX248308	EX248308 Danio rer	924	17	3.4	180460	9	CNS0518V	Human chr
852	17	3.4	172454	2	AC025008	AC025008 Homo sapi	925	17	3.4	180460	9	CNS0518V	Human chr
853	17	3.4	172454	2	AC025008	AC025008 Homo sapi	926	17	3.4	180460	9	CNS0518V	Human chr
854	17	3.4	172555	2	AC102866	AC102866 Mus muscu	927	17	3.4	180460	9	CNS0518V	Human chr
855	17	3.4	172623	2	AC118494	AC118494 Rattus no	928	17	3.4	180460	9	CNS0518V	Human chr
856	17	3.4	172845	9	AL160053	AL160053 Human DNA	929	17	3.4	180460	9	CNS0518V	Human chr
857	17	3.4	172845	9	AL160053	AL160053 Human DNA	930	17	3.4	180460	9	CNS0518V	Human chr
858	17	3.4	172945	9	AC108099	AC108099 Homo sapi	931	17	3.4	180460	9	CNS0518V	Human chr
859	17	3.4	173283	2	AC112405	AC112405 Rattus no	932	17	3.4	180460	9	CNS0518V	Human chr
860	17	3.4	173463	9	AL359092	AL359092 Human DNA	933	17	3.4	180460	9	CNS0518V	Human chr
861	17	3.4	173477	10	AL645547	AL645547 Mouse DNA	934	17	3.4	180460	9	CNS0518V	Human chr
862	17	3.4	173651	9	AC119034	AC119034 Homo sapi	935	17	3.4	180460	9	CNS0518V	Human chr
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865	17	3.4	173929	9	AC011928	AC011928 Homo sapi	938	17	3.4	180460	9	CNS0518V	Human chr
866	17	3.4	173929	9	AC011928	AC011928 Homo sapi	939	17	3.4	180460	9	CNS0518V	Human chr
867	17	3.4	174051	2	AC129072	AC129072 Felis cat	940	17	3.4	180460	9	CNS0518V	Human chr
868	17	3.4	174143	2	AC113806	AC113806 Rattus no	941	17	3.4	180460	9	CNS0518V	Human chr
869	17	3.4	174207	2	AC144848	AC144848 Mus muscu	942	17	3.4	180460	9	CNS0518V	Human chr
870	17	3.4	174290	5	EX649417	EX649417 Zebrafish	943	17	3.4	180460	9	CNS0518V	Human chr
871	17	3.4	174344	2	AC141172	AC141172 Rattus no	944	17	3.4	180460	9	CNS0518V	Human chr
872	17	3.4	174508	2	AC009436	AC009436 Homo sapi	945	17	3.4	180460	9	CNS0518V	Human chr
873	17	3.4	174665	10	AC122333	AC122333 Mus muscu	946	17	3.4	180460	9	CNS0518V	Human chr
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875	17	3.4	174933	8	CNS010155	CNS010155 Human chr	948	17	3.4	180460	9	CNS0518V	Human chr
876	17	3.4	175163	8	OSJN00155	OSJN00155 Human chr	949	17	3.4	180460	9	CNS0518V	Human chr
877	17	3.4	175177	9	AC020980	AC020980 Homo sapi	950	17	3.4	180460	9	CNS0518V	Human chr
878	17	3.4	175346	2	AC130426	AC130426 Homo sapi	951	17	3.4	180460	9	CNS0518V	Human chr

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ALIGNMENTS

RESULT 1
 LOCUS AX431553 500 bp
 DEFINITION Sequence 7 from Patent WO240679.
 ACCESSION AX431553
 VERSION AX431553.1 GI:21656357
 KEYWORDS Corynebacterium glutamicum
 ORGANISM Corynebacterium glutamicum

AX431553 linear PAT 28-JUN-2002

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 1
 CRAFTON, C.M. and Rayapati, P.J.
 Nucleotide sequences for transcriptional regulation in
 Corynebacterium glutamicum
 Patent: WO 0240679-A 7 23-MAY-2002;
 CRAFTON COREY M (US); RAYAPATI P JOHN (US)
 FEATURES
 Location/Qualifiers
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 DEFINITION Sequence 7069 from Patent EP1108790.
 ACCESSION AX127153
 VERSION AX127153.1 GI:14041141
 KEYWORDS
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 ORGANISM
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 Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.

1
 REFERENCES
 AUTHORS
 TITLE
 JOURNAL
 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
 Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.,
 Novel polynucleotides
 Patent: EP 1108790-A 7069 20-JUN-2001;
 KYOWA HAKKO KOGYO CO., LTD. (JP)


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Db 130060 GCTCCGATAAAGCCAGCCCAATATTTTCAGGAGAGATTCGCTCGCGTTTGGCGACATT 130001
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QY 382 TCGGACATAATCGGGCATAATTAAGGTGTAAACAAAGAAATCCGGGCGACAGCTCTTGTCT 441
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DEFINITION Sequence 3211 from Patent EP1108790.
ACCESSION AX123295
VERSION AX123295.1 GI:14040783

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KEYWORDS
SOURCE      Corynebacterium glutamicum
ORGANISM    Corynebacterium glutamicum
REFERENCE   1
AUTHORS     Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE       Novel polynucleotides
JOURNAL     Patent: EP 1108790-A 3211 20-JUN-2003;
            KYOWA HAKKO KOGYO CO., LTD. (JP)
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DEFINITION Novel polynucleotide.
ACCESSION BD165412
VERSION    BD165412.1 GI:27871224
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SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 1776)
AUTHORS    Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE      Novel polynucleotide
JOURNAL    Patent: JP 2002191370-A 3211 09-JUL-2002;
            KYOWA HAKKO KOGYO CO LTD
COMMENT    OS Corynebacterium glutamicum
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            PD 09-JUL-2002
            PF 15-DEC-2000 JP 2000405096
            PI SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
            PI KEIKO OCHIAI,
            PI HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
            PI OZAKI
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QY 82 GTCCTGATTAAGCCAGCGCCCATATTTGACGGAGGATTTCGCTCGGTTTGGCGACATT 141
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QY 142 CGGATCCCCGGGAAC 155
Db 131 CGGATCCCCGGGAAC 118
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ACCESSION AX763278
VERSION    AX763278.1 GI:32257846
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ORGANISM    Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE  1
AUTHORS     Zelder,O., Pompejus,M., Schroeder,H., Kroeger,B., Kloppege,C. and
            Haberhauer,G.
TITLE       Genes encoding for carbon metabolism and energy-producing proteins
JOURNAL     Patent: WO 03040291-A 95 15-MAY-2003;
            BASF AKTIENGESSELLSCHAFT (DE)
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REFERENCE	AUTHORS	TITLE
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complement(20993..22816)

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/note="Similar to N. tabacum salt-inducible protein
(gb|U08285)."
/codon_start=1
/evidence=not experimental
/protein_id="AAB60724.1"
/db_xref="GI:2160161"
/translation="MFRIELRCTLSQHPQFRASFLLTWYSQESVSAADNDPDP
VLKLSVAIRDSYKDPPELFSSFTDCPSIRKVLPSLVHVVDLHNHPLSLPQSFIF
AFFPFISSQGFRTVTFYFLARFLAVHEMFEAQSLIELVWVRKGNKSASVFIISL
VEMVTWPGFLVDALMTYDGLGFIIDAIQCFRLSRKRPDVRGCGNLLDRMMKL
NPTGTGFGYNEILDAGFPLNYVFNILMKNKCEKGNISDAQKVFDEITKESLOPTVV
SFNTLINGYCKVGNLDEGRFLKHQEKRTKRPDFTVYSALINALCKENKMGAGLFD
EMCKRGLIPVDIVFTTLHHSRNGEIDLMKESYQKMLSGLDQDPIVLYINLVNGFCK
NGDLVAARNIDVGMIRRLRPDKTYITLIDGFCRGGDVETALIRKEMDQNGIELDR
VGFSAIVCGMCKEGRVDAERALCEMLRAGIKPDDVTYTMMDAFCKGDAQTGFKLL
KEMQSDGHVPSVTYVNLNGLCKLGMKNADMLLDAMLNIGVVPDDITYNTLLGHH
RHANSSRYIQKPEIGIVADLASYSKISVNEIDRASKOHRNR"
complement(23293..24316)
/gene="F21M12.8"
complement(join(23293..23550,24080..24316))
/gene="F21M12.8"
/note="Similar to ribosomal protein L21 (gb|L38826). ESTs
gb|AA395597.gb|ATTS5197 come from this gene."
/codon_start=1
/evidence=not experimental
/protein_id="AAB60725.1"
/db_xref="GI:2160162"
/translation="MPAGHGVARTRDLFARPRKGYIPLSTYLRTRFKVGVDVVKV
NGAIHKMPHFYHGRTRINWTVKRAVSVENKQIGNRIIRKRITHRVEHVQQRCA
BEFKLRKKNDLKAANKANGETISTKQKPGKPGFVMEGMLTETVTPIDVVDNL
KGGY"
complement(24846..27004)

Query Match      4.6%; Score 23; DB 8; Length 146505;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 TTGCTGATTTCTGAGTCGCTTT 459
      |||||
DB 86781 TTGCTGATTTCTGAGTCGCTTT 86759

RESULT 9
AF302055 816 bp DNA linear INV 25-JAN-2001
LOCUS Ceratosolen constrictus cytochrome oxidase I (COI) gene, partial
DEFINITION cds; mitochondrial gene for mitochondrial product.
ACCESSION AF302055
VERSION AF302055.1 GI:11245194
KEYWORDS .
SOURCE mitochondrial Ceratosolen constrictus
ORGANISM Ceratosolen constrictus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
            Agaonidae; Agaoninae; Ceratosolen.
REFERENCE 1 (bases 1 to 816)
            West, S.A., Murray, M.G., Machado, C.A., Griffin, A.S. and Herre, E.A.
            Testing Hamilton's rule with competition between relatives
            Nature 409 (6819), 510-513 (2001)
JOURNAL MEDLINE 21074930
PUBMED 11206546
REFERENCE 2 (bases 1 to 816)
            Machado, C.A.
            Direct Submission
            Submitted (31-AUG-2000) Naos Laboratories, Smithsonian Tropical
            Research Institute, Balboa Apartado 2072, Panama
            Location/Qualifiers
            1. .816
            /organism="Ceratosolen constrictus"
            /organella="mitochondrion"
            /mol_type="genomic DNA"
            /strain="C.CONST"

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/db_xref="GI:11245195"

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CDS

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VWGHMFTGVNDVTRAFYSATWIGVPGIKVYSWCTLYGAKFKVTVPLLVFG
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GIGLQKLMQFSLFTGVNFTFPQHLGLSGMPRYSYDPDYMCKNKLISMGAL
LSFLSTAFFGIVLEALLSNRKLIFSTQWNISLEWMTYPPAEHSFDELKPVFI"

ORIGIN

Query Match 4.2%; Score 21; DB 3; Length 816;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 TGATTTTTCACAAAATAA 361

Db 722 TGATTTTTCACAAAATAA 742

RESULT 10

AF076155/C

LOCUS

DEFINITION Arabidopsis thaliana 8729 bp DNA linear PLN 02-MAR-1999
binding factor 1 (CBF1), CRT/DRE
complete cds.

ACCESSION

AF076155

VERSION

AF076155.1

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 8729)Gilmour,S.J., Zarka,D.G., Stockinger,E.J., Salazar,M.P.,
Houghton,J.M. and Thomashow,M.F.
Low temperature regulation of the Arabidopsis CBF family of AP2
transcriptional activators as an early step in cold-induced COR
gene expression
Plant J. 16 (4), 433-442 (1998)

JOURNAL

MEDLINE

PUBMED

9881163

2 (bases 1 to 8729)

Gilmour,S.J., Zarka,D.G., Stockinger,E.J., Salazar,M.P. and
Thomashow,M.F.
Direct Submission
Submitted (29-JUN-1998) Crop and Soil Sciences, Michigan State
University, East Lansing, MI 48824, USA
Location/Qualifiers
1. .8729
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Landberg erecta"
/db_xref="taxon:3702"
/chromosome="4"
/map="close to PG11 and m600"
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<1443..>2084
/gene="CBF1"
/product="CRT/DRE binding factor 1"
1443..2084
/gene="CBF1"
/notes="AP2 transcriptional activator"
/codon_start=1

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

mRNA

CDS

/product="CRT/DRE binding factor 1"
/protein_id="AAC99369.1"
/db_xref="GI:4091982"

gene

mRNA

CDS

/translation="MNSFSAESEMFGSDYEPQGGDYCPTLATSCPKPKAGKKRETR
HPYRQVRNSGRWSEVREPNNKTRILWLTGFTQTAEMAAAHDAVAALGRSACLN
FADSAWRLRIPESCAKDIOKAAEAALAFQDETCTTTTTHGLDMEETVVEAIYTP
QSEGAFYDEETMFGMPTLLDNMAEGMLLPSPVQWNHNYDEGGDGVLSWSY"
<5009..>5659
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/product="CRT/DRE binding factor 3"
5009..5659
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/note="AP2 transcriptional activator"
/codon_start=1
/product="CRT/DRE binding factor 3"
/protein_id="AAC99370.1"
/db_xref="GI:4091983"

CDS

mRNA

CDS

mRNA

CDS

mRNA

CDS

mRNA

CDS

mRNA

CDS

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ORIGIN

Query Match 4.0%; Score 20; DB 8; Length 8729;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 345 TTTTTCACAAAATAACAC 364

Db 3392 TTTTTCACAAAATAACAC 3373

RESULT 11

U88174

LOCUS

DEFINITION

U88174

ACCESSION

U88174.1

VERSION

U88174.1

KEYWORDS

HTG.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 25230)
Wilson,R.
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
95069613
PUBMED
9851916
REFERENCE
2 (bases 1 to 25230)
Scheet,P.
AUTHORS
TITLE
The sequence of C. elegans cosmid M01A10
Unpublished (2001)
JOURNAL
REFERENCE
3 (bases 1 to 25230)

U88174 25230 bp DNA linear INV 15-JUN-2003
Caenorhabditis elegans cosmid M01A10, complete sequence.

U88174

U88174.1

U88174.1

U88174.1

U88174.1

U88174.1

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U88174.1


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OLSDAASPLEGPISEAPKRIISEQKSFDAARRPOLFKTQSVWENGSLSRGDSORES
PSSGRQLNTSPSTSSQSLERSMSTQOESITSLFSIHYSKKNDSKSPCLWGTSA
GASLAINLILPDRFTSIIVAPSTVRLKQVISOQSFMDNTFCIISPASESYKEAA
KEQASDPRSLNKNVTNKASLAPQYSSIDSNDSEISQILIVAAENEVKVVALPTFSQ
LYVKQFDPIPLKATPTHIRGYPCIMLSAAGQIIMLSPLRLILQITIFHSEVID
DPLCQKFAFHGLGVNASOTEMEKYTWCSIAEQTGESLGEFVPCBEMQPKNNNS
FLKGVSSIFGQTPRNDPIDAILSENMGVKNSGVNPMSVARTIPGPSVCMQDRAQA
GVGSAGQAALQNLNTEKLNATVDATENLKNAMSLSRSTGKLYEYKKEKWN
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Complement (6159, .7146)
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7016, .7146))
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thermoautotrophicum Hypothetical protein MTH80.;
TR:026184; coded for by the following C. elegans cDNAs:
YK90b11.3, YK90b11.5, CEB5U19F, YK505g11.3"
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/db_xref="WormBase:M01A10.3"
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VALPSKLPNELKADASQRLYVFTVAKSDNAKVKPHOVFLRFVAQNGEDVVVNVDP
ANGNVYDNLVTRAKSPNLSGQFKISLLVGDYTIKPNQWPNIDIAALPVAIEPT
PKSQVQPEHNLVSHIRFQREKPSALISDLFTICLSPILLVLVMSQVQINPQNA
PASFWPFIHLVGLIGIFYFMFWQVDFMTLVGLVGLFTFVAGNRLVRAISEK
QKSE"

Query Match      4.0%; Score 20; DB 3; Length 25230;
Best Local Similarity 100.0%; Pred. No. 6.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 343 ATTTTTCACAAAATAAC 362
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Db 3828 ATTTTTCACAAAATAAC 3847

RESULT 12
AF000264 LOCUS 28577 bp DNA linear INV 13-JAN-2003
DEFINITION Caenorhabditis elegans cosmid F43E2, complete sequence.
ACCESSION AF000264
VERSION AF000264.1 GI:1947136
KEYWORDS HTG.
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 28577)
Waterston,R.
Genome sequencing of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
99069613
PUBMED 9851916
REFERENCE 2 (bases 1 to 28577)
AUTHORS Latreille,P.
TITLE The sequence of C. elegans cosmid F43E2
JOURNAL Unpublished (2001)
MEDLINE 3 (bases 1 to 28577)
PUBMED 9851916
REFERENCE 3 (bases 1 to 28577)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (bases 1 to 28577)
AUTHORS Waterston,R.
TITLE Direct Submission

```

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (05-NOV-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (03-JUL-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
6 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (05-OCT-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
7 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (22-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
8 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (11-OCT-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
9 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (19-NOV-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
10 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (09-DEC-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
11 (bases 1 to 28577)
Waterston,R.
Direct Submission

Submitted (13-JAN-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
Submitted by:

Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: rv@nemastode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclones.

For a graphical representation of this cosmid sequence and its analysis see:
http://www.wormbase.org/db/seq/sequence?name=F43E2;class=Sequence

NEIGHBORING COSMID INFORMATION

The 5' cosmid is F21D12, 1000 bp overlap; the 3' cosmid is C07D10, 200 bp overlap. Actual start of this cosmid is at base position 30292 of F21D12; actual end is at 7574 of C07D10.

NOTES:

Coding sequences below are the result of integration and manual review of the following data : computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfc.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES
source

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1. .28577
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    /chromosome="II"
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    complement (join(28. .132,182. .885,932. .1166,1216. .1782,
1832. .2016,2065. .2242))
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    /notes="contains similarity to Pfam domain PF00012 (Heat
shock hsp70 proteins); coded for by the following C.
elegans cDNAs: yk17h11.5, yk285f12.5, yk181e12.5,
yk68d12.5, cm06f6, yk34e10.3, yk34e10.5, yk127e8.5,
yk160a6.5, yk168a9.5, yk330d2.5, yk333b1.5, yk336e8.5,
yk345c11.5, yk374b4.5, yk375c10.5, yk400h2.5, yk421c2.5,
yk452h2.5, yk464b2.5, yk464b12.5, yk458e7.5, yk339f10.5,
yk414f6.5, yk320a1.5, yk464b2.3, yk415h6.3, yk345c11.3,
yk436h11.3, yk374b4.3, yk464b12.3, yk285f12.3, yk458e7.3,
yk375c10.3, yk421c2.3, yk339f10.3, yk336e8.3, yk330d2.3,
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ERNILYFDLGGTFDVSLLTIDSGVFEVLATNGDTHLGGDFDQRMVEYFIKLYKKS
GKDLKDNRAVKLRREVEKAKALSTQHQTKIEISLFDGEDFSELTITRAKFEELNM
DLFRATLVQVKVLEDADMKTIDVHILVGGSTRIPKVVQQLIKDFNGKEPGRGNGP
DEAVAGAAVQAGVIGVENTGDVLDVNLTLGIVETGVGMTKLGRNVTIPTKRS
QVFSTADSSQSAVSIVIEGERPMWNHKLGNFDVTGIPAPRGVPIQEVTFEIDVN
GILHVSADKGTGNKNTLITNDHNRSLSPEDIERMINDAKFAADQAOKEKVESRNE
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  /standard_name="F43E2.4"
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transporters); coded for by the following C. elegans
cDNAs: yk3d1.3, yk3d1.5, yk12a6.3, yk12a6.5, yk155c4.5,
yk287e1.5"
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  /protein_id="AAC71121.1"
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gene

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CDS
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gene

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CDS

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LYPGLWESVIMSLSGFTQVLVYFVFTSNPDFVHRLNTAENAGTSVTAAETV
RTEATSNVESGSSAPRAPLHKVLLRLLSYCGHQWPEASGFVLTVALARVFPN
YTAQISDINKRGIQALHSIIVLTCLTATISLFGKRGCFDYATALTALRIRLDL
FTSLRQDIAFYAVPLVGTIKAYSSFYDKISKLOQTIAETNQMAEEVSTWRTVRSF
MEKRLKRPEDRLSTLSVNRKKSIAVLYFTWNNFCDNAIIVAVFYGGHLVMTGK
MEKELITFLAYCMOLGENLYLVSYVMGLMEAVGARSKVFDLMNRKSPDFLDMQRP
FYNGNITFSHVGTTPSPRNNPVLDLTLSKGETVALVGPSSGKSSIVSLIEHFY
EPDEGSVLUDGPFKIDINHYTHQKVALVAQSPVLNGSVRHNILYGCFAEDDMIN
ESKAMNVHDFVMELEKGYDTCGEKGVQMGQKQRIARALVRNPVALILDEATSA
LQTESALVQQAALSCAQERTVIIVAHRLSTIEKANKIAIVKGCILVQMGTHTELTMD
TQGMYSLSVRQMLSAKVED"
8681..9140
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  join(8681..8755,8967..9140)
  /gene="F43E2.9"
  /standard_name="F43E2.9"
  /notes="contains similarity to Clostridium acetobutylicum
Hypothetical protein CAC2790.; TR:Q97FF0"
  /codon_start=1
  /product="Hypothetical protein F43E2.9"
  /protein_id="AAC71126.1"
  /db_xref="GI:1947142"

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Query Match      4.0%; Score 20; DB 3; Length 28577;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 339 TGTGATTTTTCACAAAAA 358
      |||||
Db 25035 TGTGATTTTTCACAAAAA 25016

```

RESULT 13

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CEC05A9/c

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LOCUS

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DEFINITION

```

```

ACCESSION

```

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VERSION

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KEYWORDS

```

```

SOURCE

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ORGANISM

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REFERENCE

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AUTHORS

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TITLE

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JOURNAL

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MEDLINE

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PUBMED

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REMARK

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REFERENCE

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AUTHORS

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TITLE

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```

JOURNAL

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COMMENT

```

none.
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
99069613
9851916
The C.elegans Sequencing Consortium.
2 (bases 1 to 34309)
Kershaw,J.K.
Direct Submission
Submitted (22-MAR-1996) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rwenematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
For a graphical representation of this sequence and its analysis
see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
name=C05A9

```


IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone C05A9. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C05A9 is at 1 in this sequence. The true right end of clone C05A9 is at 9694 in sequence CBT21E8.

The true left end of clone T21E8 is at 34209 in this sequence. The true right end of clone F31B12 is at 14854 in this sequence. The start of this sequence (1..44) overlaps with the end of sequence CEF31B12.

The end of this sequence (34209..34309) overlaps with the start of sequence CBT21E8.

```

FEATURES
    source
        Location/Qualifiers
            1..34309
                /organism="Caenorhabditis elegans"
                /mol_type="genomic DNA"
                /strain="Bristol N2"
                /db_xref="taxon:6239"
                /clone="C05A9"

```

ORIGIN

```

Query Match      4.0%; Score 20; DB 3; Length 34309;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 341 TGATTTTTCACAAAATA 360
Db 16743 TGATTTTTCACAAAATA 16724

```

RESULT 14

```

AL928690/c
LOCUS Mouse DNA sequence from clone RP23-443L19 on chromosome 2, complete
sequence.
DEFINITION
ACCESSION AL928690
VERSION AL928690.9 GI:28172233
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bates,K.
Direct Submission
Submitted (29-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 30, 2003 this sequence version replaced gi:27817374.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----

```

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep RP23-443L19 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACes3.6.

```

FEATURES
    source
        Location/Qualifiers
            1..98535
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /db_xref="taxon:10090"
                /chromosome="2"
                /clone="RP23-443L19"
                /clone_lib="RPCI-23"

```

ORIGIN

```

Query Match      4.0%; Score 20; DB 10; Length 98535;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 476 GCGAAATCAGGAAGTGGGAT 495
Db 82173 GCGAAATCAGGAAGTGGGAT 82154

```

RESULT 15

```

AC090524
LOCUS Caenorhabditis briggsae cosmid CB019H23, complete sequence.
DEFINITION
ACCESSION AC090524
VERSION AC090524.1 GI:13129527
KEYWORDS HTG.
SOURCE Caenorhabditis briggsae
ORGANISM Caenorhabditis briggsae
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 103244)
AUTHORS The C. briggsae Genome Sequencing Center.
TITLE Washington University Genome Sequencing Project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 103244)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: jspieth@watson.wustl.edu

```

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

```

FEATURES
    source
        Location/Qualifiers
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                /organism="Caenorhabditis briggsae"
                /mol_type="genomic DNA"
                /strain="Gujarat G16"
                /db_xref="taxon:6238"
                /clone="CB019H23"

```

ORIGIN

Query Match 4.0%; Score 20; DB 3; Length 103244;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAATAACA 363
|||
Db 58709 TTTTTCACAAAAATAACA 58728

Search completed: August 4, 2004, 15:11:03
Job time : 2199 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 13:24:02 ; Search time 304 Seconds
(without alignments)
6987.168 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcgc.....atcagggaagtggtatcgaaa 500

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	500	6 ABQ73179	Abq73179 C. glutam
2	275	55.0	309400	5 AAH68534	Aah68534 C. glutam
3	134	26.8	1776	5 AAH68176	Aah68176 C. glutam
4	134	26.8	1776	7 ACA01190	Aca01190 C. glutam
5	112	22.4	1084	9 ADD13410	Add13410 C. glutam
6	100	20.0	1065	4 AAF71424	Aaf71424 Corynebact
7	23	4.6	579	3 AAC48302	Aac48302 Arabidops
8	23	4.6	580	3 AAC34575	Aac34575 Arabidops
9	19	3.8	497	8 ACH39788	Ach39788 Human foe
10	19	3.8	852	7 ABT42792	Abt42792 Human neu
11	19	3.8	6971	6 ABN80060	Abn80060 Human che
12	19	3.8	15373	6 ABL32467	Ab132467 Human imm
13	18	3.6	109	4 AAK58736	Aak58736 Human imm
14	18	3.6	487	9 ADE81992	Ade81992 Arabidops
15	18	3.6	584	8 ACH25364	Ach25364 Human adu
16	18	3.6	627	6 ABQ30138	Abq30138 Oligonuc1
17	18	3.6	627	6 ABQ30139	Abq30139 Streptoco
18	18	3.6	1068	6 ABN67095	Abn67095 Streptoco
19	18	3.6	1536	3 AAC42290	Aac42290 Arabidops
20	18	3.6	2000	7 ADA71674	Ada71674 Rice gene
21	18	3.6	2127	6 ABA93636	Ab93636 Human thy
22	18	3.6	2706	5 ABX71398	Abx71398 Human tra
23	18	3.6	2713	7 ADA53828	Ada53828 Human cod

24	18	3.6	2972	4 ABL29422	Ab129422 Drosophil
25	18	3.6	3201	4 ABL29420	Ab129420 Drosophil
26	18	3.6	6158	4 ABL02028	Ab102028 Drosophil
27	18	3.6	7309	9 ADB54292	Adb54292 Pretreat
28	18	3.6	14006	6 ABL33958	Ab133958 Human imm
29	18	3.6	15424	4 ABL29522	Ab129522 Drosophil
30	18	3.6	32313	4 AAK81578	Aak81578 Human imm
31	18	3.6	110000	6 ABN71527_09	Continuation (10 o
32	17	3.4	392	4 AAL24878	Aal24878 Human bre
33	17	3.4	513	8 ACH45236	Ach45236 Human foe
34	17	3.4	557	4 ABA59682	Ab59682 Human foe
35	17	3.4	557	4 AAI139547	Aai139547 Probe #82
36	17	3.4	557	4 AAK33821	Aak33821 Human bon
37	17	3.4	557	4 AAK07951	Aak07951 Human bra
38	17	3.4	557	4 ABS33631	Ab33631 Human liv
39	17	3.4	557	6 ABS08671	Ab508671 Human gen
40	17	3.4	569	4 AAI17081	Aai17081 Probe #70
41	17	3.4	569	4 ABA61415	Ab61415 Human foe
42	17	3.4	569	4 AAI141325	Aai141325 Probe #10
43	17	3.4	569	4 ABA29177	Ab29177 Probe #76
44	17	3.4	569	4 AAK35608	Aak35608 Human bon
45	17	3.4	569	4 AAK09715	Aak09715 Human bra
46	17	3.4	569	4 ABS35332	Ab35332 Human liv
47	17	3.4	569	6 ABS09905	Ab509905 Human gen
48	17	3.4	645	2 AAV37411	Aav37411 Streptoco
49	17	3.4	696	4 AAH90744	Aah90744 CFE 48 co
50	17	3.4	720	4 AAH90857	Aah90857 2CFE 48 c
51	17	3.4	744	7 ABX07371	Abx07371 S. pneumo
52	17	3.4	791	4 AAL25020	Aal25020 Human BSK
53	17	3.4	965	9 ADE76303	Ade76303 Human BSK
54	17	3.4	1005	7 ACA43048	Aca43048 Prokaryot
55	17	3.4	1124	9 ADB69291	Adb69291 C. neofor
56	17	3.4	1170	7 ACA47870	Aca47870 Prokaryot
57	17	3.4	1243	2 AAV99106	Aav99106 DNA methy
58	17	3.4	1602	9 ADB87429	Adb87429 Transgene
59	17	3.4	2414	4 AAH15118	Aah15118 Human cDN
60	17	3.4	2546	2 AAX78320	Aax78320 A. chryso
61	17	3.4	2877	3 AAI10739	Aai10739 C. albica
62	17	3.4	3124	9 ADB68930	Adb68930 C. neofor
63	17	3.4	3128	5 AAS78582	Aas78582 DNA encod
64	17	3.4	3726	7 ACA49641	Aca49641 S. pneumo
65	17	3.4	3729	7 ACA49641	Aca49641 Prokaryot
66	17	3.4	4084	5 AAS71947	Aas71947 DNA encod
67	17	3.4	5092	4 AAI59458	Aai59458 Human pol
68	17	3.4	5290	4 ABL08212	Ab108212 Drosophil
69	17	3.4	5434	6 ABL62902	Ab162902 Breast ca
70	17	3.4	5434	6 ABL63111	Ab163111 Breast ca
71	17	3.4	5434	6 ABL64407	Ab164407 Stomach c
72	17	3.4	5434	7 ABT33842	Abt33842 DNMT1 cDN
73	17	3.4	5771	6 ABL33951	Ab133951 Human imm
74	17	3.4	5794	5 AAS78583	Aas78583 DNA encod
75	17	3.4	6069	9 ADD18703	Add18703 Human dis
76	17	3.4	7066	10 ADE77197	Ade77197 Human cDN
77	17	3.4	7514	7 ACC46596	Acc46596 Human dit
78	17	3.4	9905	6 ABL32062	Ab132062 Human imm
79	17	3.4	11443	2 AAV52182	Aav52182 Streptoco
80	17	3.4	19440	2 AAV99129	Aav99129 DNA methy
81	17	3.4	19553	4 ABK42538	Abk42538 Genomic s
82	17	3.4	19553	8 ADB60694	Adb60694 Connectiv
83	17	3.4	28473	2 AAV52216	Aav52216 Streptoco
84	17	3.4	35962	7 AB211014	Ab211014 Haematopo
85	17	3.4	96595	8 ADA02726	Ada02726 Human SYK
86	17	3.4	96595	9 ADB72464	Adb72464 Human SYK
87	17	3.4	110000	6 ABQ74964_1	Continuation (2 of
88	17	3.4	110000	7 ABS56454_14	Continuation (15 o
89	17	3.4	110000	7 ABS56454_18	Continuation (19 o
90	17	3.4	110000	7 ABS56454_20	Continuation (21 o
91	17	3.4	134525	2 AAQ04525	Aaq04525 Total bas
92	16	3.2	133	5 ABV56660	Abv56660 Human pro
93	16	3.2	146	6 ABK91750	Abk91750 DNA encod
94	16	3.2	185	4 AAS50733	Aas50733 Staphyloc
95	16	3.2	185	7 ACA18029	Aca18029 Prokaryot
96	16	3.2	210	7 ABX49361	Abx49361 Bovine ES

97	16	3.2	227	6	ABK79441	Abk79441 Bacillus	170	16	3.2	755	4	AAK75148	AAK75148 Human imm
98	16	3.2	238	3	AAC05174	Aac05174 Human sec	171	16	3.2	755	4	AAK75149	AAK75149 Human imm
99	16	3.2	246	4	AAS48802	Aas48802 Staphyloc	c 172	16	3.2	780	6	ABQ47385	Abq47385 Oligonuc1
100	16	3.2	246	4	AAS48821	Aas48821 Staphyloc	173	16	3.2	780	6	ABQ47384	Abq47384 Oligonuc1
101	16	3.2	246	4	AAS48883	Aas48883 Staphyloc	174	16	3.2	783	4	AAI95867	AAI95867 Human neu
102	16	3.2	246	4	AAS48883	Aas48883 Staphyloc	175	16	3.2	836	6	ABQ88749	Abq88749 Human pro
103	16	3.2	246	4	AAS48894	Aas48894 Staphyloc	c 176	16	3.2	844	6	ABQ88749	Abq88749 Human pro
104	16	3.2	246	4	AAS48894	Aas48894 Staphyloc	c 177	16	3.2	845	6	ABQ82705	Abq82705 Rice meva
105	16	3.2	246	4	AAS48964	Aas48964 Staphyloc	c 178	16	3.2	852	3	AAK60295	AAK60295 A. pullul
106	16	3.2	246	7	ACA16070	AcA16070 Prokaryot	c 179	16	3.2	870	7	ACA31024	AcA31024 Arabidops
107	16	3.2	246	7	ACA16135	AcA16135 Prokaryot	c 180	16	3.2	891	9	ADC74842	AdC74842 Human pro
108	16	3.2	246	7	ACA16220	AcA16220 Prokaryot	c 181	16	3.2	901	3	AAK38429	AAK38429 Arabidops
109	16	3.2	246	7	ACA16184	AcA16184 Prokaryot	182	16	3.2	915	5	ACA28096	AcA28096 Prokaryot
110	16	3.2	246	7	ACA16094	AcA16094 Prokaryot	183	16	3.2	941	4	AAK64636	AAK64636 Human imm
111	16	3.2	246	7	ACA16064	AcA16064 Prokaryot	184	16	3.2	941	7	ABX63705	ABX63705 Human cDN
112	16	3.2	247	7	ACA16145	AcA16145 Prokaryot	c 185	16	3.2	969	2	AAK61792	AAK61792 B. burgdo
113	16	3.2	252	6	ABU77028	AbU77028 Human ORF	186	16	3.2	984	4	ABU11599	ABU11599 Drosophil
114	16	3.2	267	6	ABN77263	AbN77263 Human ORF	187	16	3.2	1005	2	AAZ22857	AAZ22857 Wheat ant
115	16	3.2	300	2	AAZ12749	Aaz12749 Human gen	c 188	16	3.2	1011	5	AAZ22857	AAZ22857 Wheat ant
116	16	3.2	303	7	ACA39469	AcA39469 Prokaryot	c 189	16	3.2	1011	5	AAZ22857	AAZ22857 Wheat ant
117	16	3.2	307	3	ACA12495	AcA12495 Human sec	c 190	16	3.2	1011	5	AAZ22857	AAZ22857 Wheat ant
118	16	3.2	316	2	AAV87092	Aav87092 Bst clone	c 191	16	3.2	1037	3	AAZ22857	AAZ22857 Wheat ant
119	16	3.2	327	7	ABX53982	AbX53982 Bovine ES	c 192	16	3.2	1056	9	ACA18527	AcA18527 Prokaryot
120	16	3.2	334	3	AAA45074	Aaa45074 Human sec	193	16	3.2	1056	9	ADP78316	ADP78316 Human dit
121	16	3.2	378	4	AAI86260	Aai86260 Human pol	194	16	3.2	1065	7	ACC46280	Acc46280 Human dit
122	16	3.2	390	7	ACA73895	AcA73895 Human imm	195	16	3.2	1071	5	AAK67833	AAK67833 DNA encod
123	16	3.2	393	7	ACA30598	AcA30598 Prokaryot	196	16	3.2	1080	2	AAK67833	AAK67833 DNA encod
124	16	3.2	397	4	AAI84846	Aai84846 Human pol	c 197	16	3.2	1110	9	ADC91989	AdC91989 E. faeciu
125	16	3.2	429	7	ABX44906	AbX44906 Bovine ES	c 198	16	3.2	1134	4	AAI65118	AAI65118 Ribosomal
126	16	3.2	430	6	ABU65953	AbU65953 Lung canc	199	16	3.2	1400	3	ACG62024	AcG62024 Nucleotid
127	16	3.2	430	6	ABU65953	AbU65953 Lung canc	200	16	3.2	1410	8	ACC43044	Acc43044 Nucleotid
128	16	3.2	450	9	ADD32947	Add32947 Human mit	201	16	3.2	1410	8	ACC43044	Acc43044 Nucleotid
129	16	3.2	455	6	ACH32017	Ach32017 Human end	202	16	3.2	1410	8	ACC43044	Acc43044 Nucleotid
130	16	3.2	477	8	ACH32017	Ach32017 Human end	203	16	3.2	1410	8	ACC43044	Acc43044 Nucleotid
131	16	3.2	490	4	AAI16355	Aai16355 Probe #62	204	16	3.2	1434	6	ADP42886	ADP42886 Human DNA
132	16	3.2	490	4	ABA559201	AbA559201 Human foe	c 205	16	3.2	1458	7	ACA45761	AcA45761 Prokaryot
133	16	3.2	490	4	ABA559201	AbA559201 Human foe	206	16	3.2	1531	7	ACC78321	Acc78321 DNA encod
134	16	3.2	490	4	ABA27960	AbA27960 Probe #64	207	16	3.2	1532	4	AAI93822	AAI93822 Human pol
135	16	3.2	490	4	AAK33180	Aak33180 Human bon	208	16	3.2	1539	9	ADC93278	AdC93278 E. faeciu
136	16	3.2	490	4	AAK07403	Aak07403 Human bra	c 209	16	3.2	1547	6	ABX67092	ABX67092 Human col
137	16	3.2	490	4	ABX32926	AbX32926 Human liv	210	16	3.2	1547	6	ABT05254	ABT05254 Human col
138	16	3.2	490	6	ABS08008	AbS08008 Human gen	211	16	3.2	1547	6	ABT05254	ABT05254 Human col
139	16	3.2	497	4	AAH71718	Aah71718 Human cer	c 212	16	3.2	1547	6	ABT03032	ABT03032 Human bre
140	16	3.2	497	4	AAH72541	Aah72541 Human cer	213	16	3.2	1559	2	AAI91855	AAI91855 DUB-1 enh
141	16	3.2	510	4	AAK85709	Aak85709 Human imm	c 214	16	3.2	1577	4	AAI91855	AAI91855 DUB-1 enh
142	16	3.2	510	4	AAK85710	Aak85710 Human imm	c 215	16	3.2	1584	7	ACA23970	AcA23970 Prokaryot
143	16	3.2	527	4	AAH70286	Aah70286 Human cer	216	16	3.2	1595	7	ADP51049	ADP51049 Human DME
144	16	3.2	549	7	ACD97652	AcD97652 Human col	c 217	16	3.2	1624	4	AAI987118	AAI987118 NOV7 codi
145	16	3.2	554	4	ABA59800	AbA59800 Human foe	c 218	16	3.2	1638	7	ACA26091	AcA26091 Prokaryot
146	16	3.2	554	4	AAI39672	Aai39672 Probe #83	219	16	3.2	1657	5	ABV25742	ABV25742 Human pro
147	16	3.2	554	4	AAK33947	Aak33947 Human bon	c 220	16	3.2	1704	6	ACA24358	AcA24358 DNA encod
148	16	3.2	554	4	AAK08073	Aak08073 Human bra	c 221	16	3.2	1763	7	ACA33386	AcA33386 Prokaryot
149	16	3.2	554	4	AAK33752	Aak33752 Human liv	c 222	16	3.2	1804	4	AAI987114	AAI987114 NOV3 codi
150	16	3.2	554	6	ABS08758	AbS08758 Human gen	c 223	16	3.2	1827	6	ABN92451	ABN92451 Staphyloc
151	16	3.2	558	4	ABA62435	AbA62435 Human foe	c 224	16	3.2	1896	9	ADP93359	ADP93359 E. faeciu
152	16	3.2	558	4	ABA62435	AbA62435 Human foe	c 225	16	3.2	1944	7	ADA53840	ADa53840 Human cod
153	16	3.2	558	4	AAK10777	Aak10777 Human bra	c 226	16	3.2	1956	7	ACA54394	AcA54394 Prokaryot
154	16	3.2	558	4	ABS36305	AbS36305 Human liv	c 227	16	3.2	2000	6	ABZ17051	ABZ17051 Arabidops
155	16	3.2	558	6	ABQ27674	AbQ27674 Oligonuc1	c 228	16	3.2	2000	7	ADA69079	ADa69079 Arabidops
156	16	3.2	558	6	ABQ27675	AbQ27675 Oligonuc1	c 229	16	3.2	2010	4	AAI987118	AAI987118 NOV2 codi
157	16	3.2	558	6	ABS10651	AbS10651 Human gen	c 230	16	3.2	2010	9	ADA2808	ADa2808 Chlamydia
158	16	3.2	626	6	AAK32848	Aak32848 Human G p	c 231	16	3.2	2011	4	AAI987118	AAI987118 NOV2 codi
159	16	3.2	635	6	AAK31049	Aak31049 Plant dwa	c 232	16	3.2	2023	7	ADA53138	ADa53138 Human cod
160	16	3.2	656	6	AAK31043	Aak31043 Plant dwa	c 233	16	3.2	2026	7	ACC78319	Acc78319 DNA encod
161	16	3.2	675	7	ACA36670	AcA36670 Prokaryot	c 234	16	3.2	2089	7	ACC78320	Acc78320 DNA encod
162	16	3.2	690	7	ACF74295	AcF74295 Staphyloc	c 235	16	3.2	2177	9	ABT07590	ABT07590 Human bre
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C 583	16	3.2	2340	8	ACH06639	Human sec	ACH75931	Human sec
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C 585	16	3.2	2340	8	ACH06639	Human sec	ACH05718	CDNA enco
C 586	16	3.2	2340	8	ACH06639	Human sec	ACH2768	Human sec
C 587	16	3.2	2340	8	ACH06639	Human sec	ACH55977	Human sec
C 588	16	3.2	2340	8	ACH06639	Human sec	ACH55363	Human sec
C 589	16	3.2	2340	8	ACH06639	Human sec	ACH86076	Human sec
C 590	16	3.2	2340	8	ACH06639	Human sec	ACH56284	Human sec
C 591	16	3.2	2340	8	ACH06639	Human sec	ACH56591	Human sec
C 592	16	3.2	2340	8	ACH06639	Human sec	ACH55670	Human sec
C 593	16	3.2	2340	8	ACH06639	Human sec	ACH55056	Human sec
C 594	16	3.2	2340	8	ACH06639	Human sec	ACH18155	Human PRO
C 595	16	3.2	2340	8	ACH06639	Human sec	ACH05806	Human sec
C 596	16	3.2	2340	8	ACH06639	Human sec	ACH70801	Human CDN
C 597	16	3.2	2340	8	ACH06639	Human sec	ACH39878	Human CDN
C 598	16	3.2	2340	8	ACH06639	Human sec	ACH70324	Human CDN
C 599	16	3.2	2340	8	ACH06639	Human sec	ACH38445	Human CDN
C 600	16	3.2	2340	8	ACH06639	Human sec	ACH39401	Human CDN
C 601	16	3.2	2340	8	ACH06639	Human sec	ACH38924	Human CDN
C 602	16	3.2	2340	8	ACH06639	Human sec	ACH40355	Human CDN
C 603	16	3.2	2340	8	ACH06639	Human sec	ACH50576	Human CDN
C 604	16	3.2	2340	8	ACH06639	Human sec	ACH20188	Human CDN
C 605	16	3.2	2340	8	ACH06639	Human sec	ACH50099	Human CDN
C 606	16	3.2	2340	8	ACH06639	Human sec	ACH21657	Human CDN
C 607	16	3.2	2340	10	ACH06639	Human sec	ACH74470	Human sec

C 681	16	3.2	2340	10	AD575082	Ad575082 Human sec	C 754	16	3.2	6478	9	AD54155	Ad54155 Pretreat
C 682	16	3.2	2346	2	AAV42000	AAV42000 Nucleotid	C 755	16	3.2	6478	9	AD54283	Ad54283 Pretreat
C 683	16	3.2	2346	2	AAV42000	AAV42000 Nucleotid	C 756	16	3.2	6591	4	AA546283	AA546283 Tumour su
C 684	16	3.2	2346	6	AAK87022	AAK87022 A. hydrop	C 757	16	3.2	6626	4	AA546809	AA546809 Tumour su
C 685	16	3.2	2382	6	AAK87022	AAK87022 A. hydrop	C 758	16	3.2	7471	3	AAZ88789	AAZ88789 B. subtil
C 686	16	3.2	2409	2	AAQ12084	AAQ12084 C-termina	C 759	16	3.2	7499	1	AAZ88789	AAZ88789 B. subtil
C 687	16	3.2	2410	7	AAQ12084	AAQ12084 C-termina	C 760	16	3.2	7502	6	AAQ27429	AAQ27429 PCTD. 3/2
C 688	16	3.2	2410	9	ABT41885	ABT41885 Toxicity-	C 761	16	3.2	7603	6	ABL32308	ABL32308 Human imm
C 689	16	3.2	2410	9	ABT41885	ABT41885 Toxicity-	C 762	16	3.2	7603	6	ABL32308	ABL32308 Human imm
C 690	16	3.2	2469	4	ABL18522	ABL18522 Drosophill	C 763	16	3.2	8044	4	AA546626	AA546626 Tumour su
C 691	16	3.2	2481	5	AA570479	AA570479 DNA encod	C 764	16	3.2	8259	4	ABL16826	ABL16826 Drosophill
C 692	16	3.2	2483	4	AA570479	AA570479 DNA encod	C 765	16	3.2	8326	4	AAK90175	AAK90175 Human dig
C 693	16	3.2	2512	4	AA570479	AA570479 DNA encod	C 766	16	3.2	8326	5	AAK90175	AAK90175 Human dig
C 694	16	3.2	2512	4	AA570479	AA570479 DNA encod	C 767	16	3.2	8326	5	AAK90175	AAK90175 Human dig
C 695	16	3.2	2546	6	AAK13180	AAK13180 Enterococ	C 768	16	3.2	8326	5	AAK90175	AAK90175 Human dig
C 696	16	3.2	2546	6	AAK13180	AAK13180 Enterococ	C 769	16	3.2	8326	5	AAK90175	AAK90175 Human dig
C 697	16	3.2	2580	6	ABZ13699	ABZ13699 Arabidops	C 770	16	3.2	8807	9	AA535915	AA535915 Human nov
C 698	16	3.2	2580	6	ABZ13699	ABZ13699 Arabidops	C 771	16	3.2	8807	9	AA535915	AA535915 Human nov
C 699	16	3.2	2581	4	ABU12794	ABU12794 Drosophill	C 772	16	3.2	8990	4	AAK77783	AAK77783 Human imm
C 700	16	3.2	2631	9	ADC77525	ADC77525 Zebrafish	C 773	16	3.2	9193	6	ABL23683	ABL23683 Human imm
C 701	16	3.2	2652	4	AA506756	AA506756 Polyucle	C 774	16	3.2	9733	6	ABL23683	ABL23683 Human imm
C 702	16	3.2	2686	4	AA513465	AA513465 DNA encod	C 775	16	3.2	10312	4	AAK84424	AAK84424 Human imm
C 703	16	3.2	2688	7	ACC78318	ACC78318 DNA encod	C 776	16	3.2	10312	4	AAK84424	AAK84424 Human imm
C 704	16	3.2	2720	7	ABQ83445	ABQ83445 Human ade	C 777	16	3.2	11009	6	ABQ72907	ABQ72907 Mouse lam
C 705	16	3.2	2806	8	ABZ57829	ABZ57829 Mycobacte	C 778	16	3.2	11009	6	AAI70816	AAI70816 Mouse lam
C 706	16	3.2	3003	4	AAH54803	AAH54803 S. epidid	C 779	16	3.2	11131	4	ABL09428	ABL09428 Drosophill
C 707	16	3.2	3013	2	AAV01451	AAV01451 Plasmid p	C 780	16	3.2	11691	6	ABL34241	ABL34241 Human imm
C 708	16	3.2	3150	2	AAV05542	AAV05542 Actinobac	C 781	16	3.2	11694	4	AA546697	AA546697 Tumour su
C 709	16	3.2	3172	4	ABL04524	ABL04524 Drosophill	C 782	16	3.2	12202	4	ABL221186	ABL221186 Drosophill
C 710	16	3.2	3215	4	AA504041	AA504041 Human ABC	C 783	16	3.2	12263	6	ABK84514	ABK84514 Human cDN
C 711	16	3.2	3254	7	ABQ83446	ABQ83446 Human ade	C 784	16	3.2	12711	6	ABL34525	ABL34525 Human met
C 712	16	3.2	3260	6	ABT08489	ABT08489 Human nov	C 785	16	3.2	12711	6	ABL70250	ABL70250 Chemical
C 713	16	3.2	3572	8	ACA98949	ACA98949 cDNA enco	C 786	16	3.2	13732	6	ABL33820	ABL33820 Human imm
C 714	16	3.2	3623	4	AAI93584	AAI93584 Human pol	C 787	16	3.2	15297	7	ABA94501	ABA94501 Human pro
C 715	16	3.2	3625	4	AAI93584	AAI93584 Human pol	C 788	16	3.2	15297	7	ABV75414	ABV75414 Human kin
C 716	16	3.2	3660	9	ADB84153	ADB84153 Gene expr	C 789	16	3.2	17222	4	ABL03508	ABL03508 Drosophill
C 717	16	3.2	3723	7	ACAA4526	ACAA4526 Prokaryot	C 790	16	3.2	19211	3	AA81507	AA81507 N. mening
C 718	16	3.2	3908	4	AA225749	AA225749 Chlamydia	C 791	16	3.2	21606	4	AA536233	AA536233 Human ABC
C 719	16	3.2	3957	9	ADP42744	ADP42744 Chlamydia	C 792	16	3.2	21606	4	AA536233	AA536233 Human ABC
C 720	16	3.2	4027	4	ABL221187	ABL221187 Drosophill	C 793	16	3.2	21606	4	AA536233	AA536233 Human ABC
C 721	16	3.2	4111	5	AB83184	AB83184 HOST-5 (N	C 794	16	3.2	21732	5	AA539820	AA539820 Genomic s
C 722	16	3.2	4135	4	AA539820	AA539820 Genomic s	C 795	16	3.2	21732	5	AA539820	AA539820 Genomic s
C 723	16	3.2	4135	6	AA539820	AA539820 Genomic s	C 796	16	3.2	21732	5	AA539820	AA539820 Genomic s
C 724	16	3.2	4137	2	AA539820	AA539820 Genomic s	C 797	16	3.2	23272	8	ACC69138	ACC69138 M. genita
C 725	16	3.2	4137	3	AA539820	AA539820 Genomic s	C 798	16	3.2	23272	8	ACC69138	ACC69138 M. genita
C 726	16	3.2	4141	9	AD57243	AD57243 Rat gene	C 799	16	3.2	29596	4	ABL28638	ABL28638 Drosophill
C 727	16	3.2	4149	4	ABL02771	ABL02771 Drosophill	C 800	16	3.2	29596	4	ABL28638	ABL28638 Drosophill
C 728	16	3.2	4269	4	ABL17138	ABL17138 Drosophill	C 801	16	3.2	30143	4	ABL18564	ABL18564 Human che
C 729	16	3.2	4576	6	ABA04662	ABA04662 Human Hya	C 802	16	3.2	30143	4	ABL18564	ABL18564 Human che
C 730	16	3.2	4580	4	ABL13746	ABL13746 Drosophill	C 803	16	3.2	34548	6	ABL70603	ABL70603 Chemical
C 731	16	3.2	4603	7	ABZ09973	ABZ09973 Haematopo	C 804	16	3.2	38342	6	ABK31506	ABK31506 Signal tr
C 732	16	3.2	4603	7	ABZ09973	ABZ09973 Haematopo	C 805	16	3.2	38342	6	ABK31506	ABK31506 Signal tr
C 733	16	3.2	4603	7	ABZ09973	ABZ09973 Haematopo	C 806	16	3.2	50000	6	AA226437	AA226437 Human GRM
C 734	16	3.2	4688	7	ABK13822	ABK13822 cDNA enco	C 807	16	3.2	50000	6	AA226437	AA226437 Human GRM
C 735	16	3.2	4688	7	ABK13822	ABK13822 cDNA enco	C 808	16	3.2	50000	6	AA226437	AA226437 Human GRM
C 736	16	3.2	4688	7	ABK13822	ABK13822 cDNA enco	C 809	16	3.2	66949	6	ABQ88140	ABQ88140 Human ost
C 737	16	3.2	4835	3	AA539820	AA539820 Genomic s	C 810	16	3.2	66949	6	ABQ88140	ABQ88140 Human ost
C 738	16	3.2	4835	3	AA539820	AA539820 Genomic s	C 811	16	3.2	70768	6	AAI41152	AAI41152 Wooden le
C 739	16	3.2	4835	3	AA539820	AA539820 Genomic s	C 812	16	3.2	70768	6	AAI41152	AAI41152 Wooden le
C 740	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 813	16	3.2	72787	8	ACH03408	ACH03408 3
C 741	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 814	16	3.2	72787	8	ACH03408	ACH03408 3
C 742	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 815	16	3.2	72787	8	ACH03408	ACH03408 3
C 743	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 816	16	3.2	72787	8	ACH03408	ACH03408 3
C 744	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 817	16	3.2	72787	8	ACH03408	ACH03408 3
C 745	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 818	16	3.2	72787	8	ACH03408	ACH03408 3
C 746	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 819	16	3.2	72787	8	ACH03408	ACH03408 3
C 747	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 820	16	3.2	72787	8	ACH03408	ACH03408 3
C 748	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 821	16	3.2	72787	8	ACH03408	ACH03408 3
C 749	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 822	16	3.2	72787	8	ACH03408	ACH03408 3
C 750	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 823	16	3.2	72787	8	ACH03408	ACH03408 3
C 751	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 824	16	3.2	72787	8	ACH03408	ACH03408 3
C 752	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 825	16	3.2	72787	8	ACH03408	ACH03408 3
C 753	16	3.2	5371	2	AAV74575	AAV74575 Staphyloc	C 826	16	3.2	72787	8	ACH03408	ACH03408 3

827	16	3.2	110000	7	ACF67367_26	Continuation (27 o	C 900	15	3.0	327	2	AAV18560	Aav18560 Erwinia c
828	16	3.2	110000	7	ACF67367_27	Continuation (28 o	C 901	15	3.0	327	2	AAV18596	Aav18596 Erwinia c
829	16	3.2	110000	7	ACF67367_40	Continuation (41 o	C 902	15	3.0	327	2	AAV82359	Aav82359 DNA encod
830	16	3.2	110000	7	ACF65388_07	Continuation (8 of	C 903	15	3.0	327	9	AH22082	Aah22082 Erwinia c
831	16	3.2	110000	7	ACF65386_1	Continuation (2 of	C 904	15	3.0	327	9	AH22082	Aah22082 Erwinia c
832	16	3.2	110000	7	ACF65386_2	Continuation (3 of	C 905	15	3.0	328	3	ADC65043	Adc65043 Immunogl
833	16	3.2	110608	6	ABK83572_1	Continuation (3 of	C 906	15	3.0	329	4	AAH69435	Aah69435 Human cer
834	16	3.2	146547	7	ABZ80817	Abz80817 Human pho	C 907	15	3.0	333	6	ABN22147	Abn22147 Human ORF
835	16	3.2	167739	8	AD58258	Ad58258 Murine tu	C 908	15	3.0	333	7	ACA40978	Ac40978 Prokaryot
836	16	3.2	183999	4	AAFP2831	Aaf2831 Human ABC	C 909	15	3.0	334	6	ABZ35596	Abz35596 Human Gen
837	16	3.2	213251	6	ABQ67193	Abq67193 Listeria	C 910	15	3.0	336	7	ABX48756	Abx48756 Bovine ES
838	16	3.2	265118	5	AAH41227	Aah41227 Pyrococcu	C 911	15	3.0	336	7	ACA41920	Ac41920 Prokaryot
839	16	3.2	349980	5	AAH41227	Aah41227 Pyrococcu	C 912	15	3.0	336	7	ACA48620	Ac48620 Prokaryot
840	16	3.2	349980	3	AAH41227	Aah41227 Pyrococcu	C 913	15	3.0	338	7	ABZ72375	Abz72375 Rice leaf
841	15	3.0	51	4	AAU31171	Aal31171 Human SNP	C 914	15	3.0	341	6	ABK78233	Abk78233 Bacillus
842	15	3.0	59	3	AAAL3818	Aaal3818 Diphtheri	C 915	15	3.0	344	5	AAF67129	Aaf67129 Novel hum
843	15	3.0	59	7	ADA88975	Ada88975 S. coelic	C 916	15	3.0	347	3	AAZ28523	Aaz28523 Human sec
844	15	3.0	59	7	ADA88975	Ada88975 S. coelic	C 917	15	3.0	349	3	AAI184920	Aai184920 Human pol
845	15	3.0	59	7	ADA88977	Ada88977 S. coelic	C 918	15	3.0	351	7	ACA46803	Ac46803 Prokaryot
846	15	3.0	59	7	ADA88977	Ada88977 S. coelic	C 919	15	3.0	351	8	ADB12007	Adb12007 Alloococ
847	15	3.0	74	2	AAZ24058	Aaz24058 Human gen	C 920	15	3.0	352	4	AAI16460	Aai16460 Probe #63
848	15	3.0	90	7	ABZ79185	Abz79185 Tumour su	C 921	15	3.0	352	4	ABX59414	Abx59414 Human foe
849	15	3.0	90	7	ABZ097732	Abz097732 Human oli	C 922	15	3.0	352	4	AAI39230	Aai39230 Probe #79
850	15	3.0	100	7	ACD74569	Ac74569 E. coli K	C 923	15	3.0	352	4	ABA28085	Ab28085 Probe #65
851	15	3.0	117	2	AAQ02896	Aaq02896 Gene enco	C 924	15	3.0	352	4	AAK33454	Aak33454 Human bon
852	15	3.0	136	4	ABA70015	Ab70015 Human foe	C 925	15	3.0	352	4	AAK07646	Aak07646 Human bra
853	15	3.0	136	4	AAI50128	Aai50128 Probe #18	C 926	15	3.0	352	4	ABG33212	Abg33212 Human liv
854	15	3.0	136	4	AAK44120	Aak44120 Human bon	C 927	15	3.0	352	6	ABS08298	Abs08298 Human gen
855	15	3.0	136	4	AAK18224	Aak18224 Human bra	C 928	15	3.0	354	3	AAAS0093	Aas0093 Arabidops
856	15	3.0	136	4	ABSA3776	Ab3776 Human liv	C 929	15	3.0	354	7	ABZ38568	Abz38568 N. gonorr
857	15	3.0	136	6	ABSI18355	Ab18355 Human gen	C 930	15	3.0	364	4	AAH11550	Aah11550 Human bre
858	15	3.0	138	3	AAAC32571	Aac32571 Human sec	C 931	15	3.0	390	8	ACH29214	Ach29214 Human adu
859	15	3.0	146	2	AAV77001	Aav77001 Staphyloc	C 932	15	3.0	391	4	AAI81341	Aai81341 Human pol
860	15	3.0	149	6	ABL93149	Ab193149 Rat metas	C 933	15	3.0	393	2	AAV85536	Aav85536 EST clone
861	15	3.0	155	4	AAAS48653	Aas48653 Pseudomon	C 934	15	3.0	393	9	ADC90897	Adc90897 E. faeciu
862	15	3.0	155	4	AAAS48677	Aas48677 Pseudomon	C 935	15	3.0	396	4	AAAS60349	Aas60349 Human can
863	15	3.0	155	7	ACAI15717	Ac15717 Prokaryot	C 936	15	3.0	398	5	ABV16707	Abv16707 Human pro
864	15	3.0	165	7	ACAI15695	Ac15695 Prokaryot	C 937	15	3.0	399	8	ACH19365	Ach19365 Human adu
865	15	3.0	165	7	ACF68492	Acf68492 Photorhab	C 938	15	3.0	401	7	ABX41628	Abx41628 Bovine ES
866	15	3.0	232	3	AAAC16170	Aac16170 Human sec	C 939	15	3.0	401	8	ACH16527	Ach16527 Human adu
867	15	3.0	237	7	ABX49911	Abx49911 Bovine ES	C 940	15	3.0	402	4	AAI20448	Aai20448 Human bre
868	15	3.0	256	3	AAH11164	Aah11164 Partial h	C 941	15	3.0	402	5	AAAS75093	Aas75093 DNA encod
869	15	3.0	268	3	ABN81035	Abn81035 Shrimp po	C 942	15	3.0	403	4	AAI16177	Aai16177 Human bre
870	15	3.0	269	2	AAAT20837	Aat20837 Human gen	C 943	15	3.0	403	7	ABX38783	Abx38783 Bovine ES
871	15	3.0	271	6	ABN79571	Abn79571 Human ORF	C 944	15	3.0	405	4	AAAS60725	Aas60725 Human can
872	15	3.0	288	6	ABU71824	Ab171824 Corn tass	C 945	15	3.0	405	7	ABZ38569	Abz38569 N. gonorr
873	15	3.0	290	3	AAAC05902	Aac05902 Human sec	C 946	15	3.0	408	6	ABN19454	Abn19454 Human ORF
874	15	3.0	300	2	AAZ14921	Aaz14921 Human gen	C 947	15	3.0	410	4	AAI14598	Aai14598 Human bre
875	15	3.0	300	2	AAZ14965	Aaz14965 Human gen	C 948	15	3.0	412	7	ABX41629	Abx41629 Bovine ES
876	15	3.0	301	3	AAAO6464	Aao6464 Human imm	C 949	15	3.0	413	7	ABX48625	Abx48625 Bovine ES
877	15	3.0	301	4	AAH933580	Aah933580 Human pro	C 950	15	3.0	416	6	ABK45258	Abk45258 cDNA enco
878	15	3.0	301	4	AAAS63672	Aas63672 Human pro	C 951	15	3.0	420	4	AAAS37340	Aas37340 Novel hum
879	15	3.0	301	4	AAH02645	Aah02645 Prostate	C 952	15	3.0	428	6	ABL65118	Ab165118 Lung canc
880	15	3.0	301	4	AAH84894	Aah84894 Human pro	C 953	15	3.0	428	6	ABL64604	Ab164604 Stomach c
881	15	3.0	301	4	AAH10934	Aah10934 Human cDN	C 954	15	3.0	428	6	ABN95527	Abn95527 Gene #202
882	15	3.0	301	5	AAAS9481	Aas9481 Prostate	C 955	15	3.0	429	4	AAAL00909	Aal00909 Human rep
883	15	3.0	301	6	ABL95044	Ab195044 Human JPT	C 956	15	3.0	433	7	ACA14047	Ac14047 Prokaryot
884	15	3.0	301	7	ACC95208	Acc95208 Prostate	C 957	15	3.0	437	6	ABQ99210	Abq99210 Human ORF
885	15	3.0	301	9	ADBI3681	Adb3681 Human pro	C 958	15	3.0	439	4	ABAS30426	Aas30426 DNA encod
886	15	3.0	303	4	AAH72913	Aah72913 Human cer	C 959	15	3.0	439	4	AAAL04459	Aal04459 Human rep
887	15	3.0	303	4	AAH72313	Aah72313 Human cer	C 960	15	3.0	440	3	AAAC01475	Aac01475 Human sec
888	15	3.0	307	6	AAH70770	Aah70770 Human cer	C 961	15	3.0	444	7	ABX06836	Abx06836 S. pneumo
889	15	3.0	307	6	ABL80727	Ab180727 Human ova	C 962	15	3.0	444	7	ABX06836	Abx06836 S. pneumo
890	15	3.0	309	3	AAAC09054	Aac09054 Human sec	C 963	15	3.0	444	7	ACA27802	Ac27802 Prokaryot
891	15	3.0	312	9	ADBS1263	Adb51263 Primary r	C 964	15	3.0	447	4	AAI86120	Aai86120 Human pol
892	15	3.0	319	5	ABAI6888	Ab16888 Human ner	C 965	15	3.0	451	6	ABK39609	Abk39609 cDNA enco
893	15	3.0	319	5	ABAI6889	Ab16889 Human ner	C 966	15	3.0	451	7	ACA11938	Aca11938 Human lun
894	15	3.0	319	5	ABAI6890	Ab16890 Human ner	C 967	15	3.0	451	7	ACA03124	Aca03124 Lung canc
895	15	3.0	320	2	AAAX33648	Aax33648 DNA tande	C 968	15	3.0	453	6	ABN70560	Abn70560 Streptoco
896	15	3.0	327	1	AAAN90302	Aan90302 Pectate l	C 969	15	3.0	453	6	ABV95846	Abv95846 Human pan
897	15	3.0	327	1	AAAT51044	Aat51044 Pel B sig	C 970	15	3.0	453	6	ABV95579	Abv95579 Human pan
898	15	3.0	327	2	AAAT70874	Aat70874 Erwinia c	C 971	15	3.0	455	4	AAAS24617	Aas24617 Human ova
899	15	3.0	327	2	AAV03933	Aav03933 Erwinia c	C 972	15	3.0	455	5	AAH83240	Aah83240 Human ova

973 15 3.0 456 7 ABZ40094
 c 974 15 3.0 457 5 ABV46505
 c 975 15 3.0 458 8 ACH18286
 c 976 15 3.0 460 4 AAS60350
 c 977 15 3.0 462 3 ARA69611
 c 978 15 3.0 462 4 AAS57753
 c 979 15 3.0 462 8 ACH18278
 c 980 15 3.0 463 4 ABA57389
 c 981 15 3.0 463 4 AAI36934
 c 982 15 3.0 463 4 AAK31024
 c 983 15 3.0 463 4 AAK05425
 c 984 15 3.0 463 4 AAS30703
 c 985 15 3.0 463 6 ABS05774
 c 986 15 3.0 464 8 ACH45182
 c 987 15 3.0 468 4 AAI92974
 c 988 15 3.0 468 5 ABV12629
 c 989 15 3.0 469 4 ABA57383
 c 990 15 3.0 469 4 AAI36927
 c 991 15 3.0 469 4 AAK31017
 c 992 15 3.0 469 4 AAK05418
 c 993 15 3.0 469 4 ABS30696
 c 994 15 3.0 469 6 ABS05767
 c 995 15 3.0 470 4 AAI13970
 c 996 15 3.0 470 4 ABA55698
 c 997 15 3.0 470 4 AAI35353
 c 998 15 3.0 470 4 ABA45208
 c 999 15 3.0 470 4 ABA25385
 1000 15 3.0 470 4 AAK29393

ALIGNMENTS

RESULT 1
 ID ABQ73179 standard; DNA; 500 BP.
 XX
 AC ABQ73179;
 XX

27-SEP-2002 (first entry)
 XX

C. glutamicum transcriptional regulatory region 1dh DNA SEQ ID NO:7.
 XX

Corynebacterium glutamicum; transcriptional regulation; gene expression;
 amino acid biosynthesis; gene; ds.
 XX

Corynebacterium glutamicum.
 OS

WO200240679-A2.
 FN

23-MAY-2002.
 XX

15-NOV-2001; 2001WO-US043096.
 XX

15-NOV-2000; 2000US-0248219P.
 XX

(RAYA/) RAYAPATI P J.
 XX

(CRAF/) CRAFTON C M.
 XX

Rayapati PJ, Crafton CM;
 PI

WPI; 2002-575217/61.
 XX

Novel polynucleotides from Corynebacterium glutamicum useful for inducing
 and regulating expression of genes, including those that are involved in
 amino acid biosynthesis, in bacterial cells.
 XX

Claim 20; Page 25; 112pp; English.
 PS

The present invention describes Corynebacterium glutamicum
 CC

transcriptional regulatory region polynucleotide sequences (I). ABQ73173
 CC

to ABQ73194 represent the C. glutamicum transcriptional regulatory
 CC

regions pta, aceA, aceB, adh, aldE, poxB, ldh, amyE, malZ, bglX, gam,
 CC

CC glgX, hisD, pyrR, purD, hrcA, htpX, dnaK, etc, grpE, clpB, and nara,
 CC respectively. (I) can be used for producing a vector. (I) can also be
 CC used for producing a transformed Corynebacterium sp. host cell, which is
 CC useful for producing a biosynthetic product. (I) is useful for producing
 CC a Corynebacterium sp. host cell, which is useful for producing an amino
 CC acid. (I) is useful for regulating and enhancing the production of a
 CC variety of products in host cells, including amino acids such as lysine,
 CC purine nucleotides such as inosinic acid, and heterologous polypeptides
 XX

Seq Sequence 500 BP; 127 A; 110 C; 145 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 500; DB 6; Length 500;

Best Local Similarity 100.0%; Pred. No. 7.3e-248;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACACCGGTTTCGGCAACAATGACGGCAGAGA 60

Db 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACACCGGTTTCGGCAACAATGACGGCAGAGA 60

QY 61 GCCCACCACATTGCGATTTCGCTCCGATAAAGCCAGCGCCCATATTTGCGAGGAGGATT 120

Db 61 GCCCACCACATTGCGATTTCGCTCCGATAAAGCCAGCGCCCATATTTGCGAGGAGGATT 120

QY 121 CGCCTGCGGTTTGGCGACATTTCGGATCCCGGACACAGCTCTGCAATGACCTGCGCGCG 180

Db 121 CGCCTGCGGTTTGGCGACATTTCGGATCCCGGACACAGCTCTGCAATGACCTGCGCGCG 180

QY 181 AGGGAAGCGAGGTGGGTGGCGAGTTTGTAGTCGGGTTTAAAGCGTTGCCAGGCGAGTGGTG 240

Db 181 AGGGAAGCGAGGTGGGTGGCGAGTTTGTAGTCGGGTTTAAAGCGTTGCCAGGCGAGTGGTG 240

QY 241 AGCAAAAGCGCTAGTCTCTGGGAGCGAAACCATATTTAGATCATCTTGGCAGAGCATGCA 300

Db 241 AGCAAAAGCGCTAGTCTCTGGGAGCGAAACCATATTTAGATCATCTTGGCAGAGCATGCA 300

QY 301 ATTCGAGGCGCATAGATTGGTTTGTCTCGATTTTACATGATGATTTTCAACAAAAATA 360

Db 301 ATTCGAGGCGCATAGATTGGTTTGTCTCGATTTTACATGATGATTTTCAACAAAAATA 360

QY 361 ACATCTGCTGTACACACATTTTCGCACATATTCGGGCATATTAAGGTGTAAACAAGGA 420

Db 361 ACATCTGCTGTACACACATTTTCGCACATATTCGGGCATATTAAGGTGTAAACAAGGA 420

QY 421 ATCCGGGCACAAAGCTCTTGTGATTTTCTGAGCTGCTTTGGGTTGTCGGTTAGGAA 480

Db 421 ATCCGGGCACAAAGCTCTTGTGATTTTCTGAGCTGCTTTGGGTTGTCGGTTAGGAA 480

QY 481 ATCAGGAAGTGGGATCGAAA 500

Db 481 ATCAGGAAGTGGGATCGAAA 500

RESULT 2

AAH68534/C

ID AAH68534 standard; DNA; 309400 BP.

XX

AC AAH68534;

XX

DT 26-SEP-2001 (first entry)

XX

DE C glutamicum coding sequence fragment SEQ ID NO: 7069.

XX

KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis; ds.

XX

OS Corynebacterium glutamicum.

XX

FN EP1108790-A2.

XX

PD 20-JUN-2001.

XX

PF 18-DEC-2000; 2000EP-00127688.

XX

DT 03-JUN-2003 (first entry)
 XX C. glutamicum derived ORF SEQ ID 1181.
 XX
 KW Coryneform; nucleic acid array; fermentation; culture; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN DE10128510-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 13-JUN-2001; 2001DE-01028510.
 XX
 PR 13-JUN-2001; 2001DE-01028510.
 XX
 PA (DEGS) DEGUSSA AG.
 XX
 PI Farwick M, Moeckel B, Pfefferle W, Bathe B, Huthmacher K;
 XX WPI; 2003-279970/28.
 DR
 DR
 PT New nucleic acid array useful for monitoring mRNA expression of
 PT Corynebacterium glutamicum during fermentation, comprising nucleic acid
 PT from Corynebacterium glutamicum.
 XX
 PS Claim 1; Page 426-427; 709pp; German.
 XX
 CC This invention describes a novel nucleic acid array involving
 CC Corynebacterium glutamicum polynucleotides. The arrays are used to
 CC analyse C. glutamicum, particularly for monitoring a fermentation process
 CC to determine expression levels of C. glutamicum cellular mRNA. Such
 CC monitoring particularly differentiates between expression levels of
 CC different strains of C. glutamicum and allows the adjustment of different
 CC culture and fermentation conditions. ACA00010-ACA02188 represent C.
 CC glutamicum derived polynucleotides described in the disclosure of the
 CC invention
 CC
 SQ Sequence 1776 BP; 365 A; 505 C; 511 G; 395 T; 0 U; 0 Other;
 Query Match 26.8%; Score 134; DB 7; Length 1776;
 Best Local Similarity 100.0%; Pred. No. 8.7e-59;
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 GTAACCCACCACGGTTTCGGCAACAATGACGGCGAGAGAGCCACCAATTGGGATTTC 81
 Db 251 GTAACCCACCACGGTTTCGGCAACAATGACGGCGAGAGAGCCACCAATTGGGATTTC 192
 QY 82 GCTCCGATAAGCCAGCGCCCATATTTGCGAGGAGGATTGCTCGCGTTTGGGACATT 141
 Db 191 GCTCCGATAAGCCAGCGCCCATATTTGCGAGGAGGATTGCTCGCGTTTGGGACATT 132
 QY 142 CGGATCCCGGAAC 155
 Db 131 CGGATCCCGGAAC 118
 RESULT 5
 ADD13410
 ID ADD13410 standard; DNA; 1084 BP.
 XX
 AC ADD13410;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE C. glutamicum carbon metabolism associated DNA RXA02694.
 XX
 KW ds; gene; carbon metabolism; energy-rich molecule;
 KW oxidative phosphorylation; fine chemical; amino acid production;
 KW lysine production; nucleotide production; nucleoside production;
 KW lipid production; fatty acid production; diol production;
 KW carbohydrate production; aromatic compound production;
 KW vitamin production; co-factor production; enzyme production; food;
 XX

KW animal feed; cosmetic; pharmaceutical.
 XX
 OS Corynebacterium glutamicum.
 XX
 FH Key Location/Qualifiers
 FT CDS 101..1057
 FT /*tag= a
 XX
 PN WO2003040291-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 31-OCT-2002; 2002WO-EP012135.
 XX
 PR 05-NOV-2001; 2001DE-01054270.
 XX
 PA (BADI) BASF AG.
 XX
 PI Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopprogge C;
 PI Haberhauser G;
 XX
 DR WPI; 2003-505068/47.
 DR P-PSDB; ADD13411.
 XX
 PT New nucleic acid encoding variant forms of proteins involved in carbon
 PT compound metabolism, useful for production of fine chemicals,
 PT specifically lysine, in microorganisms.
 XX
 PS Claim 1; SEQ ID NO 95; 259pp; German.
 XX
 CC This invention describes novel polynucleotides and polypeptides
 CC associated with the metabolism of carbon compounds and generation of
 CC energy-rich molecules by oxidative phosphorylation in Corynebacterium
 CC glutamicum. The polynucleotides of the invention are isolated from a
 CC nucleic acid library of C. glutamicum then mutated at the specified
 CC positions, cloned and expressed by standard methods. Cells, especially
 CC Corynebacterium glutamicum, containing vectors that express the
 CC polynucleotides are used for production of fine chemicals, preferably
 CC amino acids and specifically lysine, but more generally nucleotides,
 CC nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, co-factors and enzymes. These are useful in the
 CC food, animal feed, cosmetics and pharmaceutical industries.
 CC Polynucleotides, optionally as primers and probes, can also be used for
 CC identification and classification of C. glutamicum and related species,
 CC e.g. for diagnosis; for genomic mapping; functional or evolutionary
 CC studies gene manipulation, and modulation of metabolic activity. Cells
 CC that contain the products of the invention may produce fine chemicals in
 CC better yields, with higher productivity and/or more efficiently.
 XX
 SQ Sequence 1084 BP; 270 A; 308 C; 285 G; 221 T; 0 U; 0 Other;
 Query Match 22.4%; Score 112; DB 9; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 2e-47;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 389 TAATCGGGCATAATTAAAGGTGTAAACAAGGAATCCGGGCACAGCTCTTGTGATTTC 448
 Db 1 TAATCGGGCATAATTAAAGGTGTAAACAAGGAATCCGGGCACAGCTCTTGTGATTTC 60
 QY 449 TGAGCTGCTTTTGGGTTTGTCCGGTTAGGGAATCAGGAATGGGATCGAAA 500
 Db 61 TGAGCTGCTTTTGGGTTTGTCCGGTTAGGGAATCAGGAATGGGATCGAAA 112
 RESULT 6
 AAF71424
 ID AAF71424 standard; DNA; 1065 BP.
 XX
 AC AAF71424;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:129.

XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX
 OS Corynebacterium glutamicum.

XX OS Corynebacterium glutamicum.

XX WO200100844-A2.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-IB000943.

XX 25-JUN-1999; 99US-0141031P.

XX 08-JUL-1999; 99DE-01031412.

XX 08-JUL-1999; 99DE-01031413.

XX 08-JUL-1999; 99DE-01031419.

XX 08-JUL-1999; 99DE-01031420.

XX 08-JUL-1999; 99DE-01031424.

XX 08-JUL-1999; 99DE-01031428.

XX 08-JUL-1999; 99DE-01031431.

XX 08-JUL-1999; 99DE-01031433.

XX 08-JUL-1999; 99DE-01031434.

XX 08-JUL-1999; 99DE-01031510.

XX 08-JUL-1999; 99DE-01031562.

XX 08-JUL-1999; 99DE-01031634.

XX 09-JUL-1999; 99DE-01032180.

XX 09-JUL-1999; 99DE-01032227.

XX 09-JUL-1999; 99DE-01032230.

XX 14-JUL-1999; 99US-0143208P.

XX 14-JUL-1999; 99DE-01032924.

XX 14-JUL-1999; 99DE-01032973.

XX 14-JUL-1999; 99DE-01033005.

XX 27-AUG-1999; 99DE-01040765.

XX 31-AUG-1999; 99US-0151572P.

XX 03-SEP-1999; 99DE-01042076.

XX 03-SEP-1999; 99DE-01042079.

XX 03-SEP-1999; 99DE-01042086.

XX 03-SEP-1999; 99DE-01042087.

XX 03-SEP-1999; 99DE-01042088.

XX 03-SEP-1999; 99DE-01042095.

XX 03-SEP-1999; 99DE-01042123.

XX 03-SEP-1999; 99DE-01042125.

XX (BADI) BASF AG.

XX Pompejus M, Kroeger B, Schroeder H, Zeider O, Haberhauer G;

XX WPI: 2001-061975/07.

XX P-PSDB; AAB79307.

XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 KW metabolism and oxidative phosphorylation protein for production or
 KW modulation of production of fine chemicals e.g. amino acids,
 KW carbohydrates or enzymes.

XX Claim 3; Page 332-333; 1246pp; English.

XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 KW metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
 CC to AAB 79633 which are involved in carbon metabolism and energy
 CC production. The C. glutamicum SMP gene can be used in vectors (II) for
 CC expression in host cells and production or modulation of production of
 CC fine chemicals, such as, an organic acid, a proteinogenic or
 CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
 CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
 CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
 CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
 CC encoded by them are used for diagnosing the presence or activity of

CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to C.
 CC glutamicum, identify and localise C. glutamicum sequences of interest, in
 CC evolutionary studies, in determining SMP protein regions required for
 CC function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH)
 XX
 SQ Sequence 1065 BP; 264 A; 304 C; 279 G; 218 T; 0 U; 0 Other;

Query Match 20.0%; Score 100; DB 4; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 3.2e-41;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 ATTAAAGGTGTAAACAAAGGAATCCGGGCACAAAGCTCTTCTGATTTCTGAGCTGCTTTG 460
 Db |||||
 QY 461 TGGGTTGTCGGTTAGGGAAATCAGGAATCGGATCGGAA 500
 Db |||||
 61 TGGGTTGTCGGTTAGGGAAATCAGGAATCGGATCGGAA 100

RESULT 7
 AAC48302

ID AAC48302 standard; DNA; 579 BP.

XX AAC48302;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 56987.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 04-MAY-1999; 99US-0132407P.

XX 30-APR-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 07-MAY-1999; 99US-0132487P.

XX 11-MAY-1999; 99US-0132863P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

XX 14-MAY-1999; 99US-0134370P.

XX 18-MAY-1999; 99US-0134768P.

PR	19-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-0135353P.	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135622P.	PR	03-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147953P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139117P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139462P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	99US-0139463P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139750P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151065P.
PR	21-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0151066P.
PR	22-JUN-1999;	99US-0139899P.	PR	27-AUG-1999;	99US-0151080P.
PR	23-JUN-1999;	99US-0140353P.	PR	30-AUG-1999;	99US-0151080P.
PR	23-JUN-1999;	99US-0140354P.	PR	31-AUG-1999;	99US-0151303P.
PR	24-JUN-1999;	99US-0140695P.	PR	01-SEP-1999;	99US-0151930P.
PR	28-JUN-1999;	99US-0140823P.	PR	07-SEP-1999;	99US-0152363P.
PR	29-JUN-1999;	99US-0140991P.	PR	10-SEP-1999;	99US-0153070P.
PR	30-JUN-1999;	99US-0141287P.	PR	13-SEP-1999;	99US-0153758P.
PR	01-JUL-1999;	99US-0141842P.	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0142154P.	PR	16-SEP-1999;	99US-0154039P.
PR	02-JUL-1999;	99US-0142055P.	PR	20-SEP-1999;	99US-0154779P.
PR	06-JUL-1999;	99US-0142390P.	PR	22-SEP-1999;	99US-0155139P.
PR	08-JUL-1999;	99US-0142803P.	PR	23-SEP-1999;	99US-0155486P.
PR	09-JUL-1999;	99US-0142920P.	PR	24-SEP-1999;	99US-0155659P.
PR	12-JUL-1999;	99US-0142877P.	PR	28-SEP-1999;	99US-0156458P.
PR	13-JUL-1999;	99US-0143542P.	PR	29-SEP-1999;	99US-0156596P.
PR	14-JUL-1999;	99US-0143624P.	PR	04-OCT-1999;	99US-0157117P.
PR	15-JUL-1999;	99US-0144005P.	PR	05-OCT-1999;	99US-0157753P.
PR	16-JUL-1999;	99US-0144085P.	PR	06-OCT-1999;	99US-0158029P.
PR	19-JUL-1999;	99US-0144332P.	PR	07-OCT-1999;	99US-0158029P.
PR	19-JUL-1999;	99US-0144325P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144331P.	PR	08-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144332P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144333P.			

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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161992P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.6%; Score 23; DB 3; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 TTGCTGATTTCTGAGCTGCTTT 459
Db 82 TTGCTGATTTCTGAGCTGCTTT 104

RESULT 8
AAC34575
ID AAC34575 standard; DNA; 580 BP.
XX
AC AAC34575;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7133.
XX
KW Hybridisation assay; Genetic mapping; Gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
FF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 16-APR-1999; 99US-0129845P.
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PR 30-APR-1999; 99US-0131449P.
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PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.
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PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
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 Query Match
 Best Local Similarity 100.0%; Pred. No. 0.19; Length 580;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 437 TTGCTGATTTTCGAGCTGCTTT 459
 DB 83 TTGCTGATTTTCGAGCTGCTTT 105
 RESULT 9
 ACH39788/C
 ID ACH39788 standard; cDNA; 497 BP.
 XX
 AC ACH39788;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human foetal brain cDNA #1155.
 XX
 KW Human; ss; sequencing by hybridisation; SHH; expressed sequence tag; EST;
 genome mapping; biodiversity; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2003073623-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 30-JUL-2001; 2001US-00918995.
 XX
 PR 30-JUL-2001; 2001US-00918995.
 XX
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 WPI; 2003-615964/58.
 XX
 PT New polynucleotide sequences obtained from various cDNA libraries, useful
 as hybridization probes, as oligomers for PCR, for chromosome and gene
 mapping, in the recombinant production of protein, or in generating
 antisense DNA or RNA.
 XX
 PS Claim 1; SEQ ID NO 27000; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising any one of
 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 determined by the technique of SHH (sequencing by hybridisation). Also
 included is a purified polypeptide comprising a sequence corresponding to
 a reading frame of the novel polynucleotide. The nucleic acid sequences
 are useful in diagnostics as expressed sequence tags (EST) for
 identifying expressed genes or for physical mapping of the human genome,
 in forensics, in assessing biodiversity, or in identifying mutations
 responsible for genetic disorders and other traits. The nucleotide
 sequences are also useful as hybridisation probes, as oligomers for PCR,
 for chromosome and gene mapping, in the recombinant production of
 protein, or in generating antisense DNA or RNA. The purified polypeptide
 is useful for generating antibodies specific for it. The present sequence
 is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 for this patent did not form part of the printed specification, but was
 obtained in electronic format directly from USPTO at
 cc seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX
 SQ Sequence 497 BP; 108 A; 135 C; 118 G; 121 T; 0 U; 15 Other;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 0.22; Length 497;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 475 AGGGAATCAGGAAGTGGG 493
 Db 96 AGGGAATCAGGAAGTGGG 78

RESULT 10

ABT42792/c
 ID ABT42792 standard; DNA; 852 BP.
 XX
 AC ABT42792;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Human neuroblastoma-related DNA sequence, SEQ ID NO:73.
 XX
 KW Human; ds; neuroblastoma; prognosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2002103017-A1.
 XX
 PD 27-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-JP005295.
 XX
 PR 31-MAY-2001; 2001JP-00163666.
 PR 24-AUG-2001; 2001JP-00255260.
 PA (CHTB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Nakagawara A;
 XX
 DR WPI; 2003-167523/16.
 XX

PT Nucleic acids isolated from neuroblastoma showing enhanced expression in
 PT human neuroblastoma with good prognosis, useful in clarifying good/poor
 PT prognosis of neuroblastoma and providing genetic data.
 XX
 PS Claim 1; Page 115-116; 444pp; Japanese.
 XX
 CC The invention comprises DNA sequences that show enhanced expression in
 CC human neuroblastoma with good prognosis. The DNA sequences of the
 CC invention are useful in clarifying good/poor prognosis of neuroblastoma.
 CC The present sequence represents a human neuroblastoma-related DNA
 CC sequence of the invention
 XX
 SQ Sequence 852 BP; 173 A; 152 C; 190 G; 198 T; 0 U; 139 Other;

Query Match 3.8%; Score 19; DB 7; Length 852;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 TTAAAGGTGTAACAAGGA 420
 Db 535 TTAAAGGTGTAACAAGGA 517

RESULT 11

ABN80060/c
 ID ABN80060 standard; DNA; 6971 BP.
 XX
 AC ABN80060;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human chemically modified disease associated gene SEQ ID NO 77.
 XX

XX Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
 KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;
 KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
 KW antidiabetic; cytosine; anticonvulsant; ds.

OS Homo sapiens.
 OS Synthetic.
 PN WO200200927-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP007536.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130908/17.
 XX

PT Novel nucleic acid useful for diagnosis and therapy of diseases
 PT associated with development genes such as diabetes, comprises a sequence
 PT of a segment of chemically pretreated DNA of genes associated with
 PT development.
 XX
 PS Claim 1; SEQ ID NO 77; 27pp; English.
 XX
 CC The invention relates to a nucleic acid (I) comprising a sequence at
 CC least 18 bases in length of a segment of chemically pretreated DNA (II)
 CC of genes associated with development selected from 87 genes listed in the
 CC specification such as ACCPN, ADFN, or AFDI and comprising one of 350
 CC sequences (ABN79984-ABN80333) or their complements. The invention is
 CC useful for the diagnosis or therapy of diseases associated with
 CC development genes, in particular disease related to homeobox containing
 CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
 CC associated with congenital heart disease, epilepsy, diseases related to
 CC histone deacetylation, Currarino syndrome, diseases related with the
 CC development of the brain and limb girdle muscular dystrophy and dwarfism.
 CC Oligomers specific to each of the genes are useful for detecting the
 CC methylation state of all CpG dinucleotides within the 350 sequences or
 CC (II) and their complementary sequences, as primer oligonucleotides for
 CC the amplification of the 350 sequences, (II) and/or their complements and
 CC as oligomer probes for detecting the cytosine methylation state and/or
 CC single nucleotide polymorphisms (SNPs). Note: The sequence data for this
 CC patent did not form part of the printed specification but is based on
 CC sequence information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 6971 BP; 1776 A; 282 C; 1775 G; 3137 T; 0 U; 1 Other;

Query Match 3.8%; Score 19; DB 6; Length 6971;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 344 TTTTTCACACAAAATAAC 362
 Db 421 TTTTTCACACAAAATAAC 403

RESULT 12

ABL32467/c
 ID ABL32467 standard; DNA; 15373 BP.
 XX
 AC ABL32467;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 440.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cytosine; cytosine; cytosine;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antarthritic; antidiabetic; antipsoriatic;
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;

KW ds.
XX Homo sapiens.
OS WO200200928-A2.
XX
FN 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP007537.
XX
XX 30-JUN-2000; 2000DE-01032529.
XX 01-SEP-2000; 2000DE-01043826.
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin X;
PI WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
XX Claim 1; SEQ ID NO 440; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
XX Sequence 15373 BP; 5097 A; 89 C; 2465 G; 7722 T; 0 U; 0 Other;
SQ

Query Match 3.8%; Score 19; DB 6; Length 15373;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAATAAAC 362
Db 2883 TTTTTCACAAATAAAC 2865

RESULT 13
AAK58736
ID AAK58736 standard; cDNA; 109 BP.
XX
XX AAK58736;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3796.
DE
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosinatic; gene therapy; vaccine; metastasis; ss.
KW
XX
XX Homo sapiens.
XX
XX WO200157182-A2.
FN
XX
XX 09-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US001354.
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XX 31-JAN-2000; 2000US-0179065P.
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XX 16-MAR-2000; 2000US-0189874P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 20-OCT-2000; 2000US-0240960P.
PR

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 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
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 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2001US-0254097P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-483426/52.
 DR P-PSDB; AAM85955.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Claim 1; SEQ ID NO 3796; 3071pp + Sequence Listing; English.
 CC
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 109 BP; 26 A; 29 C; 30 G; 23 T; 0 U; 1 Other;

Query Match 3.6%; Score 18; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 TTGCCAGCGAGTGGTGA 241
 |||||
 Db 51 TTGCCAGCGAGTGGTGA 68

RESULT 14

ADE81992

ID ADE81992 standard; cDNA; 487 BP.

XX ADE81992;

XX 29-JAN-2004 (first entry)

XX Arabidopsis thaliana expressed polynucleotide seq id 763.

XX genetically modified organism; transgenic organism; plant;
 KW inhibitor testing; activator testing; modifier testing; fungicide;
 KW insecticide; genetic function; genetic regulation; cellular metabolism;
 KW gene; ss.

XX Arabidopsis thaliana.

XX US2003115639-A1.

XX 19-JUN-2003.

XX 26-JAN-2001; 2001US-00770961.

XX 27-JAN-2000; 2000US-0178466P.

XX (GORL/) GORLACH J.

XX (ANY/) AN Y.

XX (HAMI/) HAMILTON C M.

XX (PRIC/) PRICE J L.

XX (RAIN/) RAINES T M.

XX (YUY/) YU Y.

XX (RAME/) RAMEAKA J G.

XX (PAGE/) PAGE A.

XX (MATH/) MATHW A V.

XX (LEDF/) LEDFORD B L.

XX (WOES/) WOESSNER J P.

XX (HAAS/) HAAS W D.

XX (GARC/) GARCIA C A.

XX (KEIC/) KRICKER M.

XX (SLAT/) SLATER T.

XX (DAVI/) DAVIS K R.

XX (ALLE/) ALLEN K.

XX (HOFF/) HOFFMAN N.

XX (HURB/) HURBAN P.

XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;

PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;

PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;

PI Hurban P;
 XX WPI; 2003-810930/76.
 XX
 PT Novel Arabidopsis thaliana nucleic acids useful for generating
 PT genetically modified transgenic organisms, for screening biologically
 PT active agents such as fungicides, insecticides.
 XX
 PS Claim 1; SEQ ID NO 763; 44pp; English.
 XX
 CC The invention describes a nucleic acid (I) comprising a sequence capable
 CC of hybridising under stringent conditions to any one of 999 fully defined
 CC Arabidopsis thaliana sequences (I) as given in specification e.g., 360,
 CC 1137, 455, 219, 472 nucleotides, etc, or its fragment. (I) is useful as a
 CC hybridisation probe to complementary molecules in a cDNA library. (I) is
 CC also useful for generating genetically modified and transgenic organisms,
 CC usually plant cells and plants. A protein encoded by (I) is useful in
 CC screening assays to determine the effect of candidate inhibitors,
 CC activators or modifiers of the gene product. The protein is also useful
 CC for screening biologically active agents e.g., fungicides and
 CC insecticides. A genetically modified cell, comprising an exogenous
 CC nucleic acid, where the nucleic acid comprises transcription regulatory
 CC sequences operably linked to a sequence capable of hybridising under
 CC stringent conditions to (I) is useful in the study of genetic function
 CC and regulation, for alteration of the cellular metabolism and for
 CC screening compounds that may affect the biological function of the gene
 CC or gene product. This sequence represents an Arabidopsis thaliana
 CC polynucleotide of the invention.
 XX
 SQ Sequence 487 BP; 109 A; 132 C; 96 G; 150 T; 0 U; 0 Other;
 Query Match 3.6%; Score 18; DB 9; Length 487;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 CAAGCTCTTCTGATTTT 447
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 Db 467 CAAGCTCTTCTGATTTT 484

RESULT 15
 ACH25364/c
 ID ACH25364 standard; cDNA; 584 BP.
 XX
 AC ACH25364;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human adult ovary cDNA #3744.
 XX
 KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX US2003073623-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 30-JUL-2001; 2001US-00918995.
 XX
 XX 30-JUL-2001; 2001US-00918995.
 XX
 PA (DEMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 DR
 XX

PT New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX
 PS Claim 1; SEQ ID NO 12576; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX
 SQ Sequence 584 BP; 158 A; 128 C; 122 G; 168 T; 0 U; 8 Other;
 Query Match 3.6%; Score 18; DB 8; Length 584;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 TTCTGCAGGGCATAGATT 319
 |||||
 Db 475 TTCTGCAGGGCATAGATT 458

Search completed: August 4, 2004, 14:34:52
 Job time : 353 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 14:23:12 ; Search time 65 Seconds
(without alignments)
4268.853 Million cell updates/sec

Title: US-09-987-763-7
Perfect score: 500
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Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	3.4	321	US-08-866-340-12	Sequence 12, Appl
C 2	17	3.4	1243	US-09-103-875-16	Sequence 16, Appl
C 3	17	3.4	1813	US-09-023-655-407	Sequence 407, Appl
C 4	17	3.4	7055	US-09-976-594-941	Sequence 941, Appl
C 5	17	3.4	11443	US-08-961-527-49	Sequence 49, Appl
C 6	17	3.4	28473	US-08-961-527-83	Sequence 83, Appl
C 7	17	3.4	786431	US-09-751-389-3	Sequence 3, Appl
C 8	16	3.2	201	US-09-621-976-13504	Sequence 13504, A
C 9	16	3.2	471	US-09-252-991A-4718	Sequence 4718, Ap
C 10	16	3.2	494	US-09-621-976-2247	Sequence 2247, Ap
C 11	16	3.2	612	US-09-252-991A-4793	Sequence 4793, Ap
C 12	16	3.2	657	US-09-252-991A-14857	Sequence 14857, A
C 13	16	3.2	795	US-08-969-644-15	Sequence 15, Appl
C 14	16	3.2	795	US-08-444-189-15	Sequence 15, Appl
C 15	16	3.2	795	US-08-468-544-15	Sequence 15, Appl
C 16	16	3.2	915	US-09-621-976-1179	Sequence 1179, Ap
C 17	16	3.2	954	US-09-252-991A-4820	Sequence 4820, Ap
C 18	16	3.2	1005	US-09-647-224A-5	Sequence 5, Appl
C 19	16	3.2	1037	US-09-535-008-57	Sequence 57, Appl
C 20	16	3.2	1059	US-09-134-000C-1838	Sequence 1838, Ap
C 21	16	3.2	1110	US-09-107-532A-1616	Sequence 1616, Ap
C 22	16	3.2	1164	US-09-252-991A-14503	Sequence 14503, A
C 23	16	3.2	1386	US-09-489-039A-5005	Sequence 5005, Ap
C 24	16	3.2	1539	US-09-107-532A-2905	Sequence 2905, Ap
C 25	16	3.2	1559	US-09-019-095A-7	Sequence 7, Appl
C 26	16	3.2	1827	US-09-134-001C-1914	Sequence 1914, Ap
C 27	16	3.2	1896	US-09-107-532A-2986	Sequence 2986, Ap

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16	3.2	2346	4	US-09-616-430-1	Sequence 1, Appl
16	3.2	2886	4	US-09-795-691-1	Sequence 1, Appl
16	3.2	2886	4	US-09-252-991A-4675	Sequence 4675, Ap
16	3.2	3013	2	US-09-096-982-6	Sequence 6, Appl
16	3.2	3013	2	US-08-653-650A-6	Sequence 6, Appl
16	3.2	3150	3	US-08-673-814-5	Sequence 5, Appl
16	3.2	3150	4	US-09-115-824-5	Sequence 5, Appl
16	3.2	3735	4	US-09-543-681A-2102	Sequence 2102, Ap
16	3.2	4137	4	US-09-499-964-2	Sequence 2, Appl
16	3.2	4563	4	US-09-252-991A-4765	Sequence 4765, Ap
16	3.2	5171	4	US-08-956-171E-264	Sequence 264, Ap
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16	3.2	6122	3	US-08-404-381-1	Sequence 1, Appl
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16	3.2	7502	3	US-08-444-189-6	Sequence 6, Appl
16	3.2	7502	3	US-08-468-544-6	Sequence 6, Appl
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16	3.2	20284	4	US-09-526-193A-21	Sequence 21, Appl
16	3.2	536165	4	US-09-214-808-1	Sequence 1, Appl
16	3.2	580073	4	US-08-545-528D-1	Sequence 1, Appl
16	3.2	640681	4	US-09-790-988-1	Sequence 1, Appl
16	3.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl
16	3.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl
15	3.0	59	4	US-09-408-618-17	Sequence 17, Appl
15	3.0	146	4	US-08-956-171E-2690	Sequence 2690, Ap
15	3.0	265	4	US-09-621-976-9909	Sequence 9909, Ap
15	3.0	298	4	US-08-651-155B-95	Sequence 95, Appl
15	3.0	298	4	US-09-194-036B-95	Sequence 95, Appl
15	3.0	301	4	US-09-439-313-231	Sequence 231, Appl
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15	3.0	301	4	US-09-232-149A-231	Sequence 231, Appl
15	3.0	301	4	US-09-159-812-231	Sequence 231, Appl
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15	3.0	301	4	US-09-688-489-231	Sequence 231, Appl
15	3.0	320	3	US-09-157-177-113	Sequence 113, Appl
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15	3.0	350	4	US-09-621-976-13474	Sequence 13474, A
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15	3.0	393	4	US-09-621-976-3619	Sequence 3619, Ap
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15	3.0	451	4	US-09-736-457-1647	Sequence 1647, Ap
15	3.0	451	4	US-09-614-124B-1647	Sequence 1647, Ap
15	3.0	451	4	US-09-671-325-1647	Sequence 1647, Ap
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15	3.0	480	4	US-09-352-616A-91	Sequence 91, Appl
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15	3.0	480	4	US-09-683-168A-91	Sequence 91, Appl
15	3.0	480	4	US-09-115-453-91	Sequence 91, Appl
15	3.0	480	4	US-09-688-489-91	Sequence 91, Appl
15	3.0	543	4	US-09-252-991A-6603	Sequence 6603, Ap
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15	3.0	567	4	US-09-252-991A-6719	Sequence 6719, Ap
15	3.0	585	4	US-09-252-991A-10341	Sequence 10341, A
15	3.0	601	3	US-09-030-607-192	Sequence 192, App
15	3.0	601	4	US-09-439-313-192	Sequence 192, App
15	3.0	601	4	US-09-352-616A-192	Sequence 192, App
15	3.0	601	4	US-09-232-149A-192	Sequence 192, App
15	3.0	601	4	US-09-158-812-192	Sequence 192, App
15	3.0	601	4	US-09-636-215-192	Sequence 192, App
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15	3.0	601	4	US-09-688-489-192	Sequence 192, App
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c 102	15	3.0	686	3	US-08-553-326-21	Sequence 21, Appl	c 175	15	3.0	3105	4	US-09-252-991A-10087	Sequence 10087, A
c 103	15	3.0	686	4	US-09-553-662-21	Sequence 21, Appl	c 176	15	3.0	3276	4	US-09-149-476-298	Sequence 298, App
c 104	15	3.0	686	4	US-10-062-994-21	Sequence 21, Appl	c 177	15	3.0	3435	4	US-09-252-991A-10017	Sequence 10017, A
c 105	15	3.0	688	3	US-08-988-416-905	Sequence 905, App	c 178	15	3.0	3629	1	US-08-354-618-1	Sequence 1, Appli
c 106	15	3.0	699	3	US-08-998-416-815	Sequence 815, App	c 179	15	3.0	3702	4	US-09-252-991A-6666	Sequence 6666, Ap
c 107	15	3.0	702	4	US-09-543-681A-3789	Sequence 3789, Ap	c 180	15	3.0	3725	1	US-08-155-331-12	Sequence 12, Appl
c 108	15	3.0	702	4	US-08-998-416-890	Sequence 890, App	c 181	15	3.0	3725	1	US-08-424-022-12	Sequence 12, Appl
c 109	15	3.0	741	3	US-09-107-532A-1386	Sequence 1386, App	c 182	15	3.0	3725	5	US-08-424-017B-12	Sequence 12, Appl
c 110	15	3.0	764	3	US-08-998-416-476	Sequence 476, App	c 183	15	3.0	3725	5	PCT-US93-11696-12	Sequence 50, Appl
c 111	15	3.0	771	4	US-08-328-352-3576	Sequence 3576, Ap	c 184	15	3.0	3768	4	US-09-566-921-50	Sequence 243, App
c 112	15	3.0	798	4	US-09-540-236-1365	Sequence 1365, App	c 185	15	3.0	3918	4	US-08-936-165A-243	Sequence 5, Appli
c 113	15	3.0	828	4	US-09-232-160-7	Sequence 7, Appli	c 186	15	3.0	4866	1	US-08-110-158-5	Sequence 45, Appl
c 114	15	3.0	894	4	US-08-328-352-3915	Sequence 3915, Ap	c 187	15	3.0	5000	4	US-09-302-769-45	Sequence 60, Appl
c 115	15	3.0	900	4	US-09-489-039A-4914	Sequence 4914, Ap	c 188	15	3.0	6156	4	US-10-204-708-60	Sequence 131, App
c 116	15	3.0	930	4	US-09-107-532A-2864	Sequence 2864, Ap	c 189	15	3.0	6186	4	US-08-961-527-131	Sequence 1, Appli
c 117	15	3.0	936	4	US-09-543-681A-1605	Sequence 1605, Ap	c 190	15	3.0	6220	4	US-09-600-087-1	Sequence 1, Appli
c 118	15	3.0	951	4	US-08-489-039A-488	Sequence 488, App	c 191	15	3.0	8145	4	US-08-961-527-122	Sequence 122, App
c 119	15	3.0	987	4	US-09-252-991A-6634	Sequence 6634, Ap	c 192	15	3.0	8916	4	US-09-579-181-11	Sequence 11, Appl
c 120	15	3.0	990	4	US-08-489-039A-778	Sequence 778, App	c 193	15	3.0	8930	4	US-09-077-098A-1	Sequence 1, Appli
c 121	15	3.0	996	4	US-09-252-991A-1223	Sequence 1223, Ap	c 194	15	3.0	9354	4	US-09-579-181-10	Sequence 10, Appl
c 122	15	3.0	996	4	US-09-252-991A-4945	Sequence 4945, Ap	c 195	15	3.0	11384	4	US-08-961-527-45	Sequence 45, Appl
c 123	15	3.0	1001	4	US-09-205-258-195	Sequence 195, App	c 196	15	3.0	11785	1	US-08-038-768A-4	Sequence 4, Appli
c 124	15	3.0	1008	4	US-09-252-991A-10020	Sequence 1020, A	c 197	15	3.0	11785	2	US-08-416-603-3	Sequence 3, Appli
c 125	15	3.0	1026	4	US-09-540-236-1214	Sequence 1214, Ap	c 198	15	3.0	12286	4	US-09-322-478-17	Sequence 17, Appl
c 126	15	3.0	1089	4	US-09-252-991A-1445	Sequence 1445, A	c 199	15	3.0	12571	4	US-09-322-478-20	Sequence 20, Appl
c 127	15	3.0	1113	4	US-08-489-039A-2356	Sequence 2356, Ap	c 200	15	3.0	14707	4	US-09-312-762A-3	Sequence 3, Appli
c 128	15	3.0	1155	4	US-09-252-991A-15185	Sequence 15185, A	c 201	15	3.0	20284	4	US-09-526-193A-21	Sequence 21, Appl
c 129	15	3.0	1209	4	US-09-328-352-827	Sequence 827, App	c 202	15	3.0	29793	4	US-09-302-812-38	Sequence 38, Appl
c 130	15	3.0	1263	4	US-09-322-478-5	Sequence 5, Appli	c 203	15	3.0	29793	4	US-09-511-477-38	Sequence 38, Appl
c 131	15	3.0	1296	4	US-09-252-991A-10631	Sequence 10631, A	c 204	15	3.0	29793	4	US-09-511-507-38	Sequence 38, Appl
c 132	15	3.0	1328	2	US-08-766-439-39	Sequence 39, Appl	c 205	15	3.0	34001	4	US-09-536-002-18	Sequence 18, Appl
c 133	15	3.0	1328	2	US-08-766-439-40	Sequence 40, Appl	c 206	15	3.0	35100	1	US-08-306-691B-19	Sequence 19, Appl
c 134	15	3.0	1332	4	US-09-540-236-1387	Sequence 1387, Ap	c 207	15	3.0	35100	5	PCT-US93-06251-1	Sequence 101, App
c 135	15	3.0	1362	4	US-09-322-478-32	Sequence 32, Appl	c 208	15	3.0	43795	3	US-08-742-185-101	Sequence 30, Appl
c 136	15	3.0	1365	4	US-09-328-352-838	Sequence 838, App	c 209	15	3.0	58909	4	US-09-536-002-38	Sequence 38, Appl
c 137	15	3.0	1407	3	US-08-581-148C-19	Sequence 19, Appl	c 210	15	3.0	94750	4	US-09-536-002-38	Sequence 37, Appl
c 138	15	3.0	1465	4	US-09-280-116-207	Sequence 207, App	c 211	15	3.0	99629	4	US-09-536-002-39	Sequence 39, Appl
c 139	15	3.0	1470	4	US-09-489-039A-7070	Sequence 7070, App	c 212	15	3.0	100848	4	US-09-536-002-39	Sequence 3, Appli
c 140	15	3.0	1477	4	US-09-585-173B-7	Sequence 7, Appli	c 213	15	3.0	148567	4	US-09-801-876B-3	Sequence 3, Appli
c 141	15	3.0	1503	4	US-09-328-352-4057	Sequence 4057, Ap	c 214	15	3.0	148567	4	US-10-254-869-3	Sequence 24, Appl
c 142	15	3.0	1542	4	US-09-252-991A-10809	Sequence 10809, A	c 215	15	3.0	169998	4	US-09-676-610B-24	Sequence 24, Appl
c 143	15	3.0	1553	3	US-08-492-459-21	Sequence 21, Appl	c 216	15	3.0	17496	4	US-09-877-177A-10	Sequence 10, Appl
c 144	15	3.0	1553	3	US-08-423-752-21	Sequence 21, Appl	c 217	15	3.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 145	15	3.0	1553	3	US-08-716-873-35	Sequence 35, Appl	c 218	15	3.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 146	15	3.0	1553	3	US-09-368-431-35	Sequence 35, Appl	c 219	15	3.0	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 147	15	3.0	1553	4	US-09-414-006-21	Sequence 21, Appl	c 220	15	3.0	269223	4	US-09-536-002-41	Sequence 41, Appl
c 148	15	3.0	1553	4	US-09-447-223-21	Sequence 21, Appl	c 221	15	3.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 149	15	3.0	1650	4	US-09-252-991A-1178	Sequence 1178, Ap	c 222	15	3.0	1664976	4	US-08-316-421B-1	Sequence 1, Appli
c 150	15	3.0	1879	4	US-09-833-381-97	Sequence 97, Appl	c 223	15	3.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 151	15	3.0	1917	4	US-09-252-991A-1386	Sequence 1386, Ap	c 224	15	3.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 152	15	3.0	1958	3	US-09-401-476-1	Sequence 1, Appli	c 225	15	3.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c 153	15	3.0	2004	1	US-08-232-015-1	Sequence 1, Appli	c 226	15	3.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c 154	15	3.0	2031	4	US-09-252-991A-6610	Sequence 6610, Ap	c 227	15	3.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 155	15	3.0	2040	3	US-08-581-148C-21	Sequence 21, Appl	c 228	15	3.0	4411529	3	US-09-103-840A-1	Sequence 8, Appli
c 156	15	3.0	2095	3	US-09-401-476-3	Sequence 3, Appli	c 229	14	2.8	22	4	US-09-769-482-8	Sequence 9, Appli
c 157	15	3.0	2217	4	US-09-107-532A-2564	Sequence 2564, Ap	c 230	14	2.8	32	2	US-08-369-829A-9	Sequence 13, Appl
c 158	15	3.0	2274	3	US-08-492-459-13	Sequence 13, Appl	c 231	14	2.8	32	2	US-08-586-676E-13	Sequence 26, Appl
c 159	15	3.0	2274	3	US-08-423-752-13	Sequence 13, Appl	c 232	14	2.8	42	1	US-08-331-398A-26	Sequence 26, Appl
c 160	15	3.0	2274	3	US-08-716-873-27	Sequence 27, Appl	c 233	14	2.8	42	2	US-08-331-397B-26	Sequence 26, Appl
c 161	15	3.0	2274	3	US-09-368-431-27	Sequence 27, Appl	c 234	14	2.8	42	2	US-08-759-804A-26	Sequence 26, Appl
c 162	15	3.0	2274	4	US-09-414-006-13	Sequence 13, Appl	c 235	14	2.8	42	3	US-09-227-693-26	Sequence 26, Appl
c 163	15	3.0	2274	4	US-09-447-223-13	Sequence 13, Appl	c 236	14	2.8	45	2	US-08-184-009-91	Sequence 91, Appl
c 164	15	3.0	2349	4	US-09-252-991A-4983	Sequence 4983, Ap	c 237	14	2.8	45	2	US-08-458-356-91	Sequence 162, App
c 165	15	3.0	2419	4	US-09-624-693A-12	Sequence 12, Appl	c 238	14	2.8	45	3	US-08-796-101-162	Sequence 91, Appl
c 166	15	3.0	2457	4	US-09-328-352-1082	Sequence 1082, Ap	c 239	14	2.8	45	3	US-08-460-736-91	Sequence 91, Appl
c 167	15	3.0	2539	3	US-08-581-148C-20	Sequence 20, Appl	c 240	14	2.8	45	4	US-09-535-370-91	Sequence 77, Appl
c 168	15	3.0	2539	3	US-09-620-312D-454	Sequence 454, App	c 241	14	2.8	48	1	US-08-208-886C-77	Sequence 77, Appl
c 169	15	3.0	2572	3	US-08-976-255-1	Sequence 1, Appli	c 242	14	2.8	48	1	US-08-704-744-77	Sequence 77, Appl
c 170	15	3.0	2684	1	US-08-367-227-1	Sequence 1, Appli	c 243	14	2.8	51	4	US-09-029-228-7	Sequence 78, Appl
c 171	15	3.0	2686	3	US-08-952-365-5	Sequence 5, Appli	c 244	14	2.8	52	1	US-08-208-886C-78	Sequence 78, Appl
c 172	15	3.0	2932	3	US-08-999-774A-5	Sequence 5, Appli	c 245	14	2.8	52	1	US-08-704-744-78	Sequence 78, Appl
c 173	15	3.0	2933	4	US-09-149-476-165	Sequence 165, App	c 246	14	2.8	79	3	US-09-449-293-2	Sequence 2, Appli

c 247	14	2.8	79	4	US-09-775-325-2	Sequence 2, Appli	c 320	14	2.8	543	4	US-09-671-325-1394	Sequence 1394, Ap
c 248	14	2.8	79	4	US-09-775-174-2	Sequence 2, Appli	321	14	2.8	544	4	US-09-634-238-147	Sequence 147, Ap
c 249	14	2.8	126	3	US-08-905-223-67	Sequence 67, Appl	322	14	2.8	546	4	US-09-621-976-2129	Sequence 2129, Ap
c 250	14	2.8	130	1	US-08-305-699-9	Sequence 9, Appli	323	14	2.8	550	4	US-09-669-751-226	Sequence 226, Ap
c 251	14	2.8	137	1	US-08-299-498A-19	Sequence 19, Appl	324	14	2.8	555	4	US-09-552-322-9	Sequence 9, Appli
c 252	14	2.8	137	5	PCT-US95-10813-19	Sequence 19, Appl	c 325	14	2.8	558	4	US-09-252-991A-14289	Sequence 14289, A
c 253	14	2.8	154	2	US-08-533-996A-1	Sequence 1, Appli	c 326	14	2.8	562	5	PCT-US92-03993-6	Sequence 6, Appli
c 254	14	2.8	178	3	US-08-991-789A-210	Sequence 210, App	c 327	14	2.8	564	4	US-09-252-991A-1261	Sequence 1261, Ap
c 255	14	2.8	178	4	US-09-062-451-210	Sequence 210, App	c 328	14	2.8	568	4	US-09-621-976-1733	Sequence 1733, Ap
c 256	14	2.8	178	4	US-09-598-326-210	Sequence 210, App	c 329	14	2.8	570	1	US-07-822-966B-1	Sequence 1, Appli
c 257	14	2.8	178	4	US-09-289-198-210	Sequence 210, App	c 330	14	2.8	578	3	US-09-328-111-742	Sequence 742, App
c 258	14	2.8	178	4	US-09-429-755-210	Sequence 210, App	c 331	14	2.8	604	4	US-09-342-653-3	Sequence 3, Appli
c 259	14	2.8	185	3	US-08-480-640A-156	Sequence 156, App	c 332	14	2.8	609	4	US-09-252-991A-8982	Sequence 8982, Ap
c 260	14	2.8	185	3	US-08-295-802-156	Sequence 156, App	c 333	14	2.8	627	3	US-08-361-441B-4	Sequence 4, Appli
c 261	14	2.8	185	3	US-08-488-237A-156	Sequence 156, App	c 334	14	2.8	628	4	US-09-221-017B-79	Sequence 79, Appl
c 262	14	2.8	185	4	US-08-375-992A-156	Sequence 156, App	c 335	14	2.8	633	4	US-09-252-991A-8508	Sequence 8508, Ap
c 263	14	2.8	185	4	US-08-472-679H-156	Sequence 156, App	c 336	14	2.8	636	4	US-09-489-039A-2437	Sequence 2437, Ap
c 264	14	2.8	196	4	US-09-313-294A-5796	Sequence 5796, Ap	c 337	14	2.8	646	4	US-09-016-434-1385	Sequence 1385, Ap
c 265	14	2.8	198	4	US-09-328-352-3145	Sequence 3145, Ap	c 338	14	2.8	651	1	US-08-171-385-4	Sequence 4, Appli
c 266	14	2.8	198	4	US-09-328-352-3560	Sequence 3560, Ap	c 339	14	2.8	654	4	US-09-252-991A-2446	Sequence 2446, Ap
c 267	14	2.8	218	4	US-09-506-729-61	Sequence 61, Appl	c 340	14	2.8	654	4	US-09-252-991A-12606	Sequence 12606, A
c 268	14	2.8	221	3	US-09-060-756-584	Sequence 584, App	c 341	14	2.8	654	4	US-09-328-352-1232	Sequence 1232, Ap
c 269	14	2.8	221	4	US-09-670-314-584	Sequence 584, App	c 342	14	2.8	666	4	US-09-543-681A-147	Sequence 147, App
c 270	14	2.8	234	4	US-09-489-039A-3210	Sequence 3210, Ap	c 343	14	2.8	678	2	US-08-951-871-3	Sequence 3, Appli
c 271	14	2.8	237	4	US-09-489-039A-5342	Sequence 5342, Ap	c 344	14	2.8	681	4	US-09-107-532A-1586	Sequence 1586, Ap
c 272	14	2.8	271	4	US-09-313-294A-5134	Sequence 5134, Ap	c 345	14	2.8	681	4	US-09-328-352-1437	Sequence 1437, Ap
c 273	14	2.8	276	4	US-09-252-991A-15626	Sequence 15626, A	c 346	14	2.8	696	4	US-09-489-039A-2440	Sequence 2440, Ap
c 274	14	2.8	278	4	US-09-621-976-10330	Sequence 10330, A	c 347	14	2.8	699	4	US-09-252-991A-4020	Sequence 4020, Ap
c 275	14	2.8	285	4	US-09-252-991A-11646	Sequence 11646, A	c 348	14	2.8	699	4	US-09-252-991A-14260	Sequence 14260, A
c 276	14	2.8	288	3	US-09-025-151-29	Sequence 29, Appl	c 349	14	2.8	707	3	US-08-998-416-876	Sequence 876, App
c 277	14	2.8	288	4	US-09-637-204-29	Sequence 29, Appl	c 350	14	2.8	720	4	US-09-252-991A-8875	Sequence 8875, Ap
c 278	14	2.8	293	4	US-09-313-294A-4949	Sequence 4949, Ap	c 351	14	2.8	720	4	US-09-489-039A-396	Sequence 396, App
c 279	14	2.8	310	4	US-09-313-294A-6506	Sequence 6506, Ap	c 352	14	2.8	720	4	US-09-134-000C-32	Sequence 32, Appl
c 280	14	2.8	315	4	US-09-489-039A-5096	Sequence 5096, Ap	c 353	14	2.8	724	4	US-09-328-475C-291	Sequence 291, App
c 281	14	2.8	321	4	US-09-252-991A-6442	Sequence 6442, Ap	c 354	14	2.8	729	4	US-09-252-991A-11790	Sequence 11790, A
c 282	14	2.8	322	1	US-09-985-799-61	Sequence 61, Appl	c 355	14	2.8	736	3	US-08-998-416-875	Sequence 875, App
c 283	14	2.8	322	1	US-08-594-031-61	Sequence 61, Appl	c 356	14	2.8	740	4	US-09-328-475C-290	Sequence 290, App
c 284	14	2.8	330	4	US-09-341-444A-3	Sequence 3, Appli	c 357	14	2.8	741	4	US-09-134-001C-1950	Sequence 1950, Ap
c 285	14	2.8	354	4	US-09-453-702B-80	Sequence 80, Appl	c 358	14	2.8	741	4	US-09-252-991A-11040	Sequence 11040, A
c 286	14	2.8	361	4	US-09-590-759-110	Sequence 110, App	c 359	14	2.8	744	4	US-09-540-236-987	Sequence 987, App
c 287	14	2.8	383	4	US-09-636-213-693	Sequence 693, App	c 360	14	2.8	746	4	US-09-902-331B-15	Sequence 15, Appl
c 288	14	2.8	383	4	US-09-685-166A-693	Sequence 693, App	c 361	14	2.8	748	3	US-09-154-083-1	Sequence 1, Appli
c 289	14	2.8	384	4	US-09-590-759-111	Sequence 111, App	c 362	14	2.8	750	4	US-09-489-039A-5270	Sequence 5270, Ap
c 290	14	2.8	385	4	US-09-392-184-23	Sequence 23, Appl	c 363	14	2.8	753	3	US-09-154-083-28	Sequence 28, Appl
c 291	14	2.8	404	1	US-09-985-799-154	Sequence 154, App	c 364	14	2.8	753	4	US-09-489-039A-1736	Sequence 1736, Ap
c 292	14	2.8	404	1	US-08-594-031-154	Sequence 154, App	c 365	14	2.8	759	4	US-09-769-482-2	Sequence 2, Appli
c 293	14	2.8	410	4	US-09-341-444A-1	Sequence 1, Appli	c 366	14	2.8	762	4	US-09-252-991A-7992	Sequence 7992, Ap
c 294	14	2.8	426	4	US-08-956-171E-694	Sequence 694, App	c 367	14	2.8	763	4	US-09-976-594-1070	Sequence 1070, Ap
c 295	14	2.8	435	1	US-08-208-886C-79	Sequence 79, Appl	c 368	14	2.8	769	4	US-08-858-207A-146	Sequence 146, App
c 296	14	2.8	435	1	US-08-704-744-79	Sequence 79, Appl	c 369	14	2.8	771	4	US-09-489-039A-5488	Sequence 5488, Ap
c 297	14	2.8	441	4	US-09-134-000C-1585	Sequence 1585, Ap	c 370	14	2.8	789	4	US-09-702-705-214	Sequence 214, App
c 298	14	2.8	447	4	US-09-252-991A-11703	Sequence 11703, A	c 371	14	2.8	789	4	US-09-736-457-214	Sequence 214, App
c 299	14	2.8	450	4	US-09-252-991A-8210	Sequence 8210, Ap	c 372	14	2.8	789	4	US-09-489-039A-4757	Sequence 4757, Ap
c 300	14	2.8	450	4	US-09-252-991A-12041	Sequence 12041, Ap	c 373	14	2.8	789	4	US-09-614-124B-214	Sequence 214, App
c 301	14	2.8	451	4	US-09-621-976-16268	Sequence 16268, A	c 374	14	2.8	789	4	US-09-671-325-214	Sequence 214, App
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c 303	14	2.8	468	4	US-09-621-976-2410	Sequence 2410, Ap	c 376	14	2.8	801	4	US-09-543-681A-2922	Sequence 2922, Ap
c 304	14	2.8	478	4	US-09-621-976-10978	Sequence 10978, A	c 377	14	2.8	807	4	US-09-328-352-455	Sequence 455, App
c 305	14	2.8	478	4	US-09-621-976-13008	Sequence 13008, A	c 378	14	2.8	807	4	US-09-107-532A-2403	Sequence 2403, Ap
c 306	14	2.8	484	4	US-09-643-597-198	Sequence 198, App	c 379	14	2.8	819	4	US-09-489-039A-3592	Sequence 3592, Ap
c 307	14	2.8	484	4	US-09-480-884A-198	Sequence 198, App	c 380	14	2.8	834	4	US-09-134-000C-753	Sequence 753, App
c 308	14	2.8	484	4	US-09-542-615A-198	Sequence 198, App	c 381	14	2.8	845	2	US-08-266-451B-1	Sequence 1, Appli
c 309	14	2.8	484	4	US-09-606-421B-198	Sequence 198, App	c 382	14	2.8	845	2	US-08-748-725-1	Sequence 1, Appli
c 310	14	2.8	486	4	US-09-621-976-3282	Sequence 3282, Ap	c 383	14	2.8	846	4	US-09-252-991A-8327	Sequence 8327, Ap
c 311	14	2.8	487	4	US-08-956-171E-547	Sequence 547, App	c 384	14	2.8	851	3	US-08-998-416-294	Sequence 294, App
c 312	14	2.8	520	4	US-09-621-976-767	Sequence 767, App	c 385	14	2.8	854	4	US-09-401-064-329	Sequence 329, App
c 313	14	2.8	525	4	US-09-833-381-945	Sequence 945, App	c 386	14	2.8	860	4	US-09-833-381-303	Sequence 303, App
c 314	14	2.8	535	4	US-09-833-381-560	Sequence 560, App	c 387	14	2.8	870	4	US-08-956-171E-879	Sequence 879, App
c 315	14	2.8	537	4	US-09-976-594-135	Sequence 135, App	c 388	14	2.8	886	4	US-09-325-932A-94	Sequence 94, Appl
c 316	14	2.8	543	4	US-09-702-705-1394	Sequence 1394, Ap	c 389	14	2.8	891	4	US-09-535-909-13	Sequence 13, Appl
c 317	14	2.8	543	4	US-09-736-457-1394	Sequence 1394, Ap	c 390	14	2.8	891	4	US-09-543-681A-204	Sequence 204, App
c 318	14	2.8	543	4	US-09-134-000C-1295	Sequence 1295, Ap	c 391	14	2.8	891	4	US-09-543-681A-1919	Sequence 1919, Ap
c 319	14	2.8	543	4	US-09-614-124B-1394	Sequence 1394, Ap	c 392	14	2.8	891	4	US-09-540-236-923	Sequence 923, App

393	14	2.8	894	4	US-09-252-991A-6276	Sequence 6276, Ap	c 466	14	2.8	1446	4	US-09-252-991A-11593	Sequence 11593, A
394	14	2.8	900	4	US-09-050-739-65	Sequence 65, Appl	467	14	2.8	1458	4	US-09-489-039A-5036	Sequence 5036, Ap
C 395	14	2.8	915	4	US-09-489-039A-5405	Sequence 5405, Ap	C 468	14	2.8	1461	4	US-09-134-000C-987	Sequence 987, App
C 396	14	2.8	917	4	US-09-976-594-483	Sequence 483, App	C 469	14	2.8	1464	4	US-09-107-532A-1565	Sequence 1565, Ap
C 397	14	2.8	921	4	US-09-023-555-401	Sequence 401, App	C 470	14	2.8	1473	4	US-09-252-991A-2391	Sequence 2391, Ap
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C 399	14	2.8	961	5	PCT-US91-08177-14	Sequence 14, Appl	C 472	14	2.8	1512	4	US-09-543-681A-39	Sequence 39, Appl
C 400	14	2.8	968	4	US-09-252-991A-13988	Sequence 13988, A	C 473	14	2.8	1519	4	US-10-024-427-3	Sequence 32, Appl
C 401	14	2.8	1001	4	US-09-671-317-89	Sequence 89, Appl	C 474	14	2.8	1521	4	US-09-540-236-322	Sequence 322, Ap
C 402	14	2.8	1002	4	US-09-252-991A-11214	Sequence 11214, A	C 475	14	2.8	1524	4	US-09-252-991A-6970	Sequence 6970, Ap
C 403	14	2.8	1005	4	US-09-134-000C-337	Sequence 337, App	476	14	2.8	1528	2	US-08-945-296-3	Sequence 3, Appli
C 404	14	2.8	1029	4	US-09-540-236-1285	Sequence 1285, Ap	477	14	2.8	1538	3	US-09-405-112-3	Sequence 3, Appli
C 405	14	2.8	1032	4	US-09-266-965-33	Sequence 33, Appl	C 478	14	2.8	1536	4	US-09-489-039A-7086	Sequence 7086, Ap
C 406	14	2.8	1035	4	US-09-489-039A-2467	Sequence 2467, Ap	479	14	2.8	1546	4	US-09-383-318A-1	Sequence 1, Appli
C 407	14	2.8	1035	4	US-09-134-000C-1789	Sequence 1789, Ap	C 480	14	2.8	1551	4	US-09-543-681A-1213	Sequence 1213, Ap
C 408	14	2.8	1038	4	US-09-540-236-1341	Sequence 1341, Ap	481	14	2.8	1566	4	US-09-252-991A-8520	Sequence 8520, Ap
C 409	14	2.8	1050	4	US-09-252-991A-6362	Sequence 6362, Ap	482	14	2.8	1575	3	US-09-230-388-2	Sequence 2, Appli
C 410	14	2.8	1053	4	US-09-107-532A-2650	Sequence 2650, Ap	483	14	2.8	1575	4	US-09-912-176-2	Sequence 2, Appli
C 411	14	2.8	1068	4	US-09-134-000C-808	Sequence 808, App	484	14	2.8	1588	1	US-08-706-037-24	Sequence 24, Appl
C 412	14	2.8	1080	4	US-09-328-352-2971	Sequence 2971, Ap	485	14	2.8	1588	2	US-09-005-397-24	Sequence 6324, Ap
C 413	14	2.8	1086	4	US-09-134-000C-1759	Sequence 1759, Ap	486	14	2.8	1611	4	US-09-252-991A-6924	Sequence 6924, Ap
C 414	14	2.8	1089	4	US-09-071-035-377	Sequence 377, App	C 487	14	2.8	1623	4	US-09-252-991A-6729	Sequence 6729, Ap
C 415	14	2.8	1090	3	US-09-124-758-1	Sequence 1, Appli	488	14	2.8	1623	4	US-09-252-991A-9839	Sequence 9839, Ap
C 416	14	2.8	1090	4	US-09-768-677-1	Sequence 1, Appli	C 489	14	2.8	1635	3	US-09-234-332-4	Sequence 4, Appli
C 417	14	2.8	1107	4	US-09-252-991A-456	Sequence 456, App	C 490	14	2.8	1635	4	US-09-702-705-1798	Sequence 1798, Ap
C 418	14	2.8	1122	4	US-09-134-000C-1964	Sequence 1964, Ap	C 491	14	2.8	1635	4	US-09-736-457-1798	Sequence 1798, Ap
C 419	14	2.8	1125	4	US-09-540-236-310	Sequence 310, App	C 492	14	2.8	1635	4	US-09-671-325-1798	Sequence 1798, Ap
C 420	14	2.8	1134	4	US-09-622-439-21	Sequence 21, Appl	C 493	14	2.8	1647	4	US-09-107-532A-2973	Sequence 2973, Ap
C 421	14	2.8	1134	4	US-09-491-577-83	Sequence 83, Appl	C 494	14	2.8	1665	4	US-09-252-991A-14320	Sequence 14320, A
C 422	14	2.8	1137	4	US-09-540-236-763	Sequence 763, App	C 495	14	2.8	1671	4	US-09-543-681A-1663	Sequence 1663, Ap
C 423	14	2.8	1140	4	US-09-769-482-1	Sequence 1, Appli	496	14	2.8	1672	1	US-08-172-331B-13	Sequence 13, Appl
C 424	14	2.8	1151	3	US-09-221-298-8	Sequence 8, Appli	C 497	14	2.8	1677	4	US-09-328-352-1861	Sequence 1861, Ap
C 425	14	2.8	1154	4	US-09-401-064-8	Sequence 8, Appli	C 498	14	2.8	1695	5	PCT-US96-05320A-265	Sequence 265, App
C 426	14	2.8	1154	4	US-09-636-382A-1	Sequence 1, Appli	C 499	14	2.8	1713	4	US-09-252-991A-109	Sequence 109, App
C 427	14	2.8	1155	2	US-09-540-236-1516	Sequence 1516, Ap	C 500	14	2.8	1713	4	US-09-489-039A-157	Sequence 157, App
C 428	14	2.8	1176	2	US-08-923-856-2	Sequence 2, Appli	C 501	14	2.8	1782	4	US-09-252-991A-6769	Sequence 6769, Ap
C 429	14	2.8	1176	3	US-09-216-294-2	Sequence 2, Appli	C 502	14	2.8	1782	4	US-09-252-991A-15714	Sequence 15714, A
C 430	14	2.8	1212	4	US-09-489-039A-5241	Sequence 5241, Ap	C 503	14	2.8	1790	4	US-09-133-962A-7	Sequence 7, Appli
C 431	14	2.8	1218	4	US-09-489-039A-42	Sequence 42, Appl	C 504	14	2.8	1794	4	US-09-252-991A-5181	Sequence 5181, Ap
C 432	14	2.8	1221	4	US-09-252-991A-2125	Sequence 2125, Ap	C 505	14	2.8	1806	4	US-09-252-991A-2306	Sequence 2306, Ap
C 433	14	2.8	1221	4	US-09-328-352-3564	Sequence 3564, Ap	C 506	14	2.8	1811	4	US-09-535-909-3	Sequence 3, Appli
C 434	14	2.8	1222	4	US-08-956-171E-13	Sequence 13, Appl	C 507	14	2.8	1822	4	US-09-833-381-1063	Sequence 1063, Ap
C 435	14	2.8	1230	3	US-09-232-479-22	Sequence 22, Appl	C 508	14	2.8	1843	4	US-09-807-258-3	Sequence 3, Appli
C 436	14	2.8	1230	4	US-09-784-990-22	Sequence 22, Appl	C 509	14	2.8	1896	4	US-09-134-000C-2770	Sequence 2770, Ap
C 437	14	2.8	1242	4	US-09-799-978-31	Sequence 31, Appl	C 510	14	2.8	1908	1	US-08-173-508-1	Sequence 1, Appli
C 438	14	2.8	1248	4	US-09-252-991A-9193	Sequence 9193, Ap	C 511	14	2.8	1908	1	US-08-173-508-1	Sequence 1, Appli
C 439	14	2.8	1251	3	US-09-007-476-1	Sequence 1, Appli	C 512	14	2.8	1908	2	US-08-265-310-1	Sequence 1, Appli
C 440	14	2.8	1251	4	US-09-620-312D-947	Sequence 947, App	C 513	14	2.8	1908	3	US-08-265-310-1	Sequence 1, Appli
C 441	14	2.8	1257	4	US-09-252-991A-14147	Sequence 14147, A	C 514	14	2.8	1908	3	US-08-951-742-1	Sequence 1, Appli
C 442	14	2.8	1260	4	US-09-252-991A-11855	Sequence 11855, A	C 515	14	2.8	1908	3	US-08-951-742-1	Sequence 1, Appli
C 443	14	2.8	1275	4	US-09-252-991A-516	Sequence 516, App	C 516	14	2.8	1931	4	US-09-220-132-1	Sequence 1, Appli
C 444	14	2.8	1278	4	US-10-024-427-1	Sequence 1, Appli	C 517	14	2.8	1932	3	US-09-232-191-32	Sequence 32, Appl
C 445	14	2.8	1284	4	US-09-894-844-106	Sequence 106, App	C 518	14	2.8	1932	3	US-09-232-200-82	Sequence 82, Appl
C 446	14	2.8	1287	4	US-09-134-000C-3052	Sequence 3052, Ap	C 519	14	2.8	1932	4	US-09-232-197-82	Sequence 82, Appl
C 447	14	2.8	1317	4	US-09-252-991A-11011	Sequence 11011, A	C 520	14	2.8	1932	4	US-09-232-195-82	Sequence 82, Appl
C 448	14	2.8	1322	4	US-09-579-236-3	Sequence 3, Appli	C 521	14	2.8	1934	4	US-09-232-195-82	Sequence 1, Appli
C 449	14	2.8	1326	4	US-09-252-991A-409	Sequence 409, App	C 522	14	2.8	1945	3	US-09-579-236-1	Sequence 77, Appl
C 450	14	2.8	1331	4	US-09-976-594-702	Sequence 702, App	C 523	14	2.8	1945	3	US-08-714-918-77	Sequence 77, Appl
C 451	14	2.8	1333	3	US-09-142-551A-1	Sequence 1, Appli	C 524	14	2.8	1945	3	US-09-265-315-77	Sequence 77, Appl
C 452	14	2.8	1338	4	US-08-887-534A-60	Sequence 60, Appl	C 525	14	2.8	1945	3	US-09-265-315-77	Sequence 77, Appl
C 453	14	2.8	1338	4	US-09-527-431-60	Sequence 60, Appl	C 526	14	2.8	1945	3	US-09-266-417-77	Sequence 77, Appl
C 454	14	2.8	1344	4	US-09-252-991A-5239	Sequence 5239, Ap	C 527	14	2.8	1945	4	US-09-527-745-77	Sequence 77, Appl
C 455	14	2.8	1345	4	US-09-976-594-239	Sequence 239, App	C 528	14	2.8	1945	4	US-09-527-745-77	Sequence 77, Appl
C 456	14	2.8	1353	4	US-09-252-991A-3984	Sequence 3984, Ap	C 529	14	2.8	1964	1	US-08-132-168A-31	Sequence 31, Appl
C 457	14	2.8	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	C 530	14	2.8	1995	4	US-09-107-532A-3598	Sequence 3598, Ap
C 458	14	2.8	1371	4	US-09-976-594-608	Sequence 608, App	C 531	14	2.8	1998	4	US-09-252-991A-6189	Sequence 6189, Ap
C 459	14	2.8	1386	4	US-09-489-039A-4802	Sequence 4802, Ap	C 532	14	2.8	2031	4	US-09-252-991A-8142	Sequence 8142, Ap
C 460	14	2.8	1392	5	PCT-US96-05320A-300	Sequence 300, App	C 533	14	2.8	2034	4	US-09-328-352-3700	Sequence 3700, Ap
C 461	14	2.8	1401	4	US-09-252-991A-10908	Sequence 10908, A	C 534	14	2.8	2118	4	US-09-252-991A-11782	Sequence 11782, A
C 462	14	2.8	1401	4	US-09-543-681A-531	Sequence 531, App	C 535	14	2.8	2133	4	US-09-164-034B-1	Sequence 15, Appl
C 463	14	2.8	1422	4	US-09-134-000C-2035	Sequence 2035, Ap	C 536	14	2.8	2138	4	US-09-747-259-15	Sequence 3, Appli
C 464	14	2.8	1425	4	US-09-252-991A-11848	Sequence 11848, A	C 537	14	2.8	2149	1	US-08-784-651-3	Sequence 294, App
C 465	14	2.8	1435	2	US-08-955-713-3	Sequence 3, Appli	C 538	14	2.8	2154	4	US-09-495-050A-294	Sequence 294, App

C 539	14	2.8	2168	1	US-08-784-651-1	Sequence 1, Appl	C 612	14	2.8	2865	4	US-09-252-991A-16281	Sequence 16281, A
540	14	2.8	2184	4	US-09-540-236-1103	Sequence 1103, Ap	C 613	14	2.8	2871	4	US-09-489-847-111	Sequence 111, App
C 541	14	2.8	2191	4	US-09-071-035-363	Sequence 363, App	C 614	14	2.8	2874	4	US-09-252-991A-15997	Sequence 15997, A
542	14	2.8	2200	4	US-09-134-001C-749	Sequence 749, App	C 615	14	2.8	2876	4	US-09-489-847-22	Sequence 22, Appl
C 543	14	2.8	2234	1	US-08-261-822A-7	Sequence 7, Appl	C 616	14	2.8	2876	4	US-09-543-681A-2235	Sequence 2235, Ap
C 544	14	2.8	2234	5	PCT-US95-07744A-7	Sequence 7, Appl	C 617	14	2.8	2910	1	US-08-375-709-6	Sequence 6, Appl
545	14	2.8	2257	4	US-09-016-434-1300	Sequence 1300, Ap	C 618	14	2.8	2910	1	US-08-752-929-6	Sequence 81, Appl
546	14	2.8	2285	1	US-08-477-674-9	Sequence 9, Appl	C 619	14	2.8	2910	1	US-09-231-899-81	Sequence 81, Appl
547	14	2.8	2285	2	US-08-473-791-9	Sequence 9, Appl	C 620	14	2.8	2928	4	US-09-328-352-638	Sequence 638, App
548	14	2.8	2285	2	US-08-316-714-9	Sequence 9, Appl	C 621	14	2.8	2929	4	US-09-543-084A-31	Sequence 31, Appl
549	14	2.8	2285	3	US-08-473-673-9	Sequence 9, Appl	C 622	14	2.8	2967	4	US-09-694-777A-14	Sequence 14, Appl
C 550	14	2.8	2292	4	US-09-107-532A-1177	Sequence 1177, Ap	C 623	14	2.8	2973	4	US-09-133-962A-15	Sequence 15, Appl
C 551	14	2.8	2331	4	US-09-134-000C-2312	Sequence 2312, Ap	C 624	14	2.8	3001	4	US-09-539-333D-174	Sequence 174, App
C 552	14	2.8	2334	4	US-09-071-035-361	Sequence 361, App	C 625	14	2.8	3001	4	US-09-539-333D-175	Sequence 175, App
C 553	14	2.8	2339	4	US-08-858-207A-47	Sequence 47, Appl	C 626	14	2.8	3051	4	US-09-409-604-1	Sequence 1, Appl
554	14	2.8	2358	1	US-08-339-152A-15	Sequence 15, Appl	C 627	14	2.8	3072	4	US-09-221-017B-337	Sequence 337, App
555	14	2.8	2358	2	US-08-007-999B-2	Sequence 2, Appl	C 628	14	2.8	3083	4	US-09-694-777A-2	Sequence 2, Appl
556	14	2.8	2358	2	US-08-689-276A-2	Sequence 2, Appl	C 629	14	2.8	3132	4	US-09-252-991A-15639	Sequence 15639, A
C 557	14	2.8	2360	1	US-08-145-681-1	Sequence 1, Appl	C 630	14	2.8	3136	4	US-09-751-389-1	Sequence 1, Appl
C 558	14	2.8	2360	1	US-08-250-308-1	Sequence 1, Appl	C 631	14	2.8	3144	2	US-08-687-916-15	Sequence 15, Appl
C 559	14	2.8	2360	2	US-08-453-703-1	Sequence 1, Appl	C 632	14	2.8	3144	3	US-09-138-614-15	Sequence 15, Appl
C 560	14	2.8	2360	2	US-08-456-106-1	Sequence 1, Appl	C 633	14	2.8	3145	4	US-09-221-017B-855	Sequence 855, App
C 561	14	2.8	2360	3	US-08-456-108-1	Sequence 1, Appl	C 634	14	2.8	3162	4	US-09-252-991A-8094	Sequence 8094, Ap
C 562	14	2.8	2360	3	US-09-265-577-1	Sequence 1, Appl	C 635	14	2.8	3168	2	US-08-659-251-14	Sequence 14, Appl
C 563	14	2.8	2360	4	US-09-633-733-1	Sequence 1, Appl	C 636	14	2.8	3168	3	US-09-256-490-14	Sequence 14, Appl
C 564	14	2.8	2360	5	PCT-US93-03614-1	Sequence 1, Appl	C 637	14	2.8	3168	5	PCT-US96-11445-14	Sequence 14, Appl
C 565	14	2.8	2367	4	US-09-252-991A-11973	Sequence 11973, A	C 638	14	2.8	3193	4	US-09-543-084A-30	Sequence 30, Appl
C 566	14	2.8	2382	4	US-09-252-991A-16507	Sequence 16507, A	C 639	14	2.8	3220	4	US-10-004-542-5	Sequence 5, Appl
567	14	2.8	2387	4	US-08-705-477E-100	Sequence 100, App	C 640	14	2.8	3222	1	US-09-543-084A-29	Sequence 29, Appl
568	14	2.8	2423	3	US-08-419-810-11	Sequence 11, Appl	C 641	14	2.8	3223	4	US-07-980-528-1	Sequence 1, Appl
569	14	2.8	2423	6	5405775-10	Patent No. 5405775	C 642	14	2.8	3233	3	US-08-755-587-43	Sequence 43, Appl
C 570	14	2.8	2432	1	US-08-078-683A-1	Sequence 1, Appl	C 643	14	2.8	3242	4	US-09-493-914-2	Sequence 2, Appl
C 571	14	2.8	2432	4	US-08-471-970A-1	Sequence 1, Appl	C 644	14	2.8	3252	4	US-08-476-102A-4	Sequence 4, Appl
C 572	14	2.8	2437	3	US-08-904-284-6	Sequence 6, Appl	C 645	14	2.8	3252	5	PCT-US96-05320A-714	Sequence 714, App
C 573	14	2.8	2439	4	US-09-252-991A-1957	Sequence 1957, Ap	C 646	14	2.8	3255	4	US-09-601-198-108	Sequence 108, App
C 574	14	2.8	2463	4	US-09-614-912-85	Sequence 85, Appl	C 647	14	2.8	3264	4	US-09-252-991A-12013	Sequence 12013, A
C 575	14	2.8	2481	4	US-09-016-434-1088	Sequence 1088, Ap	C 648	14	2.8	3279	4	US-09-252-991A-11905	Sequence 11905, A
C 576	14	2.8	2487	4	US-09-252-991A-14985	Sequence 14985, A	C 649	14	2.8	3404	4	US-09-453-702B-94	Sequence 94, Appl
577	14	2.8	2547	4	US-09-252-991A-5294	Sequence 5294, Ap	C 650	14	2.8	3422	3	US-09-586-719-26	Sequence 26, Appl
C 578	14	2.8	2554	4	US-09-620-312D-377	Sequence 377, App	C 651	14	2.8	3453	3	US-09-139-064-1	Sequence 1, Appl
C 579	14	2.8	2571	4	US-09-134-001C-2601	Sequence 2601, Ap	C 652	14	2.8	3453	3	US-09-139-064-3	Sequence 3, Appl
C 580	14	2.8	2583	4	US-09-252-991A-9110	Sequence 9110, Ap	C 653	14	2.8	3453	3	US-09-139-064-5	Sequence 5, Appl
581	14	2.8	2601	4	US-09-252-991A-11077	Sequence 11077, A	C 654	14	2.8	3453	3	US-09-487-370-1	Sequence 1, Appl
C 582	14	2.8	2610	4	US-09-252-991A-11177	Sequence 11177, A	C 655	14	2.8	3453	3	US-09-487-370-3	Sequence 3, Appl
C 583	14	2.8	2622	4	US-09-489-039A-4584	Sequence 4584, Ap	C 656	14	2.8	3453	3	US-09-487-370-5	Sequence 5, Appl
584	14	2.8	2652	4	US-09-543-681A-2440	Sequence 2440, Ap	C 657	14	2.8	3462	4	US-09-362-842-7	Sequence 7, Appl
C 585	14	2.8	2653	1	US-08-325-553-1	Sequence 1, Appl	C 658	14	2.8	3495	1	US-07-828-788A-13	Sequence 13, Appl
586	14	2.8	2653	2	US-08-394-152A-1	Sequence 1, Appl	C 659	14	2.8	3495	1	US-08-356-034-3	Sequence 3, Appl
587	14	2.8	2653	4	US-08-705-477B-1	Sequence 1, Appl	C 660	14	2.8	3495	3	US-08-933-891-3	Sequence 3, Appl
C 588	14	2.8	2674	4	US-09-817-180-1	Sequence 1, Appl	C 661	14	2.8	3495	4	US-09-521-344-3	Sequence 3, Appl
C 589	14	2.8	2674	4	US-10-003-295-1	Sequence 1, Appl	C 662	14	2.8	3495	5	PCT-US92-11337-13	Sequence 13, Appl
C 590	14	2.8	2675	1	US-08-070-165F-5	Sequence 5, Appl	C 663	14	2.8	3495	6	5188960-3	Patent No. 5188960
C 591	14	2.8	2675	2	US-08-885-418-5	Sequence 5, Appl	C 664	14	2.8	3528	4	US-09-252-991A-9473	Sequence 9473, Ap
C 592	14	2.8	2681	1	US-08-070-165F-9	Sequence 9, Appl	C 665	14	2.8	3573	4	US-09-252-991A-4903	Sequence 4903, Ap
C 593	14	2.8	2681	2	US-08-885-418-9	Sequence 9, Appl	C 666	14	2.8	3576	4	US-09-540-236-982	Sequence 982, App
C 594	14	2.8	2688	4	US-09-489-039A-5328	Sequence 5328, Ap	C 667	14	2.8	3607	4	US-09-563-269-17	Sequence 17, Appl
595	14	2.8	2712	4	US-09-252-991A-8406	Sequence 8406, Ap	C 668	14	2.8	3744	2	US-08-348-353-16	Sequence 16, Appl
C 596	14	2.8	2723	1	US-08-961-527-273	Sequence 273, App	C 669	14	2.8	3744	3	US-08-465-965-16	Sequence 16, Appl
C 597	14	2.8	2733	1	US-08-676-967-3	Sequence 3, Appl	C 670	14	2.8	3744	3	US-08-465-966-16	Sequence 16, Appl
C 598	14	2.8	2733	2	US-08-676-974-3	Sequence 3, Appl	C 671	14	2.8	3747	2	US-09-080-897-1	Sequence 1, Appl
C 599	14	2.8	2733	2	US-09-098-487-3	Sequence 3, Appl	C 672	14	2.8	3747	3	US-09-323-735-1	Sequence 1, Appl
600	14	2.8	2739	4	US-09-540-236-40	Sequence 40, Appl	C 673	14	2.8	3803	1	US-08-485-618-52	Sequence 52, Appl
601	14	2.8	2758	4	US-09-221-017B-441	Sequence 441, App	C 674	14	2.8	3803	1	US-08-362-652-52	Sequence 52, Appl
602	14	2.8	2788	4	US-09-221-017B-644	Sequence 644, App	C 675	14	2.8	3803	1	US-08-605-672-52	Sequence 52, Appl
C 603	14	2.8	2797	2	US-09-021-323-2	Sequence 2, Appl	C 676	14	2.8	3803	2	US-08-483-293A-52	Sequence 52, Appl
C 604	14	2.8	2815	3	US-09-276-531-127	Sequence 127, App	C 677	14	2.8	3803	2	US-08-943-633-52	Sequence 52, Appl
C 605	14	2.8	2829	4	US-10-004-543-1	Sequence 1, Appl	C 678	14	2.8	3803	3	US-09-193-043-52	Sequence 52, Appl
606	14	2.8	2831	4	US-09-477-135A-117	Sequence 117, App	C 679	14	2.8	3803	4	US-09-688-307A-52	Sequence 52, Appl
607	14	2.8	2852	4	US-09-056-556-203	Sequence 203, App	C 680	14	2.8	3803	4	US-09-350-259-52	Sequence 52, Appl
608	14	2.8	2852	4	US-09-072-596-198	Sequence 198, App	C 681	14	2.8	3833	1	US-08-917-320-18	Sequence 18, Appl
609	14	2.8	2852	4	US-09-072-967-203	Sequence 203, App	C 682	14	2.8	3833	5	PCT-US95-04611A-18	Sequence 18, Appl
C 610	14	2.8	2855	4	US-09-904-420A-1	Sequence 1, Appl	C 683	14	2.8	3889	2	US-08-648-298-1	Sequence 1, Appl
611	14	2.8	2859	4	US-09-328-352-425	Sequence 425, App	C 684	14	2.8	3896	4	US-09-795-926-44	Sequence 44, Appl

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686	14	2.8	3903	3	US-09-176-320-5	Sequence 5, Appli	c 759	14	2.8	10754	3	US-09-342-353-1	Sequence 1, Appli
687	14	2.8	4026	4	US-09-252-991A-10214	Sequence 10214, A	c 760	14	2.8	10953	4	US-08-956-171B-62	Sequence 62, Appl
688	14	2.8	4039	4	US-09-205-448-7	Sequence 7, Appli	c 761	14	2.8	11049	4	US-10-204-708-21	Sequence 21, Appl
689	14	2.8	4030	4	US-09-543-084A-26	Sequence 26, Appl	c 762	14	2.8	11049	4	US-10-204-708-21	Sequence 21, Appl
690	14	2.8	4061	3	US-08-425-843-1	Sequence 1, Appli	c 763	14	2.8	11219	1	US-07-642-734C-1	Sequence 1, Appli
691	14	2.8	4078	4	US-09-016-434-1120	Sequence 1120, Ap	c 764	14	2.8	11219	3	US-08-439-009A-1	Sequence 1, Appli
692	14	2.8	4080	4	US-09-016-434-1342	Sequence 1342, Ap	c 765	14	2.8	11272	4	US-09-341-461-1	Sequence 1, Appli
693	14	2.8	4093	4	US-09-543-084A-28	Sequence 28, Appl	c 766	14	2.8	11340	2	US-08-961-527-147	Sequence 147, App
694	14	2.8	4101	4	US-09-543-084A-27	Sequence 27, Appl	c 767	14	2.8	11385	2	US-08-639-501-1	Sequence 1, Appli
695	14	2.8	4117	4	US-08-961-527-100	Sequence 100, App	c 768	14	2.8	11385	3	US-09-044-946-1	Sequence 1, Appli
696	14	2.8	4138	1	US-08-447-411-75	Sequence 75, Appl	c 769	14	2.8	11385	3	US-09-044-946-1	Sequence 1, Appli
697	14	2.8	4138	2	US-08-662-227-33	Sequence 33, Appl	c 770	14	2.8	12145	3	US-08-968-563-19	Sequence 19, Appl
698	14	2.8	4138	4	US-09-017-947-33	Sequence 33, Appl	c 771	14	2.8	12145	3	US-08-969-683A-19	Sequence 19, Appl
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700	14	2.8	4146	1	US-08-261-822A-15	Sequence 15, Appl	c 773	14	2.8	12145	4	US-09-307-973A-10	Sequence 10, Appl
701	14	2.8	4146	5	PCT-US95-0774A-15	Sequence 15, Appl	c 774	14	2.8	12145	4	US-09-641-652-1	Sequence 1, Appli
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703	14	2.8	4197	4	US-09-543-681A-1469	Sequence 1469, Ap	c 776	14	2.8	13104	4	US-08-961-527-34	Sequence 34, Appl
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706	14	2.8	4206	4	US-09-911-781-2	Sequence 2, Appli	c 779	14	2.8	15378	3	US-08-785-420-1	Sequence 1, Appli
707	14	2.8	4352	4	US-09-620-312D-555	Sequence 555, App	c 780	14	2.8	15766	3	US-09-338-907-73	Sequence 73, Appl
708	14	2.8	4414	5	PCT-US95-04567-1	Sequence 1, Appli	c 781	14	2.8	15766	4	US-09-218-207-73	Sequence 73, Appl
709	14	2.8	4436	4	US-09-491-356C-6	Sequence 6, Appli	c 782	14	2.8	15788	4	US-09-920-759-13	Sequence 13, Appl
710	14	2.8	4495	2	US-08-849-480A-3	Sequence 3, Appli	c 783	14	2.8	16995	4	US-08-961-527-82	Sequence 82, Appl
711	14	2.8	4530	4	US-09-566-921-134	Sequence 134, App	c 784	14	2.8	17710	4	US-08-976-259-70	Sequence 70, Appl
712	14	2.8	4656	3	US-09-425-665-1	Sequence 1, Appli	c 785	14	2.8	18312	4	US-09-266-965-96	Sequence 96, Appl
713	14	2.8	4656	4	US-09-685-668-1	Sequence 1, Appli	c 786	14	2.8	19124	2	US-08-487-826B-13	Sequence 13, Appl
714	14	2.8	4768	4	US-09-526-193A-16	Sequence 16, Appl	c 787	14	2.8	19513	4	US-10-204-708-40	Sequence 40, Appl
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716	14	2.8	4898	4	US-09-636-499-17	Sequence 17, Appl	c 789	14	2.8	20303	4	US-09-596-002-12	Sequence 12, Appl
717	14	2.8	5028	4	US-09-540-236-74	Sequence 74, Appl	c 790	14	2.8	26664	4	US-09-564-805-28	Sequence 28, Appl
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726	14	2.8	5385	4	US-08-483-101-1	Sequence 1, Appli	c 799	14	2.8	32998	4	US-09-408-020-1	Sequence 1, Appli
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728	14	2.8	5577	4	US-07-841-655-1	Sequence 1, Appli	c 801	14	2.8	34794	4	US-10-002-720-44	Sequence 44, Appl
729	14	2.8	5595	1	US-07-635-965C-1	Sequence 1, Appli	c 802	14	2.8	35100	2	US-08-770-379-17	Sequence 17, Appl
730	14	2.8	5595	2	US-08-483-101-1	Sequence 1, Appli	c 803	14	2.8	35100	3	US-08-757-669A-17	Sequence 17, Appl
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733	14	2.8	5924	1	US-08-447-411-44	Sequence 44, Appl	c 806	14	2.8	36159	4	US-09-749-588-3	Sequence 3, Appli
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739	14	2.8	6203	4	US-09-134-218-3	Sequence 3, Appli	c 812	14	2.8	37950	3	US-09-338-907-183	Sequence 183, App
740	14	2.8	6203	4	US-08-961-527-155	Sequence 155, App	c 813	14	2.8	37950	4	US-09-218-207-183	Sequence 183, App
741	14	2.8	6474	4	US-09-221-017B-543	Sequence 543, App	c 814	14	2.8	38584	4	US-09-453-702B-50	Sequence 50, Appl
742	14	2.8	6496	4	US-09-252-991A-1219	Sequence 1219, Ap	c 815	14	2.8	40000	4	US-09-780-049-18	Sequence 18, Appl
743	14	2.8	6858	4	US-09-962-665-2	Sequence 2, Appli	c 816	14	2.8	40123	4	US-08-311-731A-137	Sequence 137, App
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749	14	2.8	8043	4	US-08-576-626A-2	Sequence 2, Appli	c 822	14	2.8	51259	3	US-08-781-891-209	Sequence 209, App
750	14	2.8	8051	2	US-08-961-527-123	Sequence 98, Appl	c 823	14	2.8	51259	3	US-08-781-891-209	Sequence 209, App
751	14	2.8	8697	4	US-08-961-527-123	Sequence 123, App	c 824	14	2.8	51259	4	US-09-618-166-209	Sequence 209, App
752	14	2.8	10163	2	US-08-659-251-1	Sequence 1, Appli	c 825	14	2.8	51259	4	US-09-618-166-209	Sequence 209, App
753	14	2.8	10163	3	US-09-256-490-1	Sequence 1, Appli	c 826	14	2.8	53500	4	US-09-266-965-76	Sequence 76, Appl
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755	14	2.8	10163	5	US-10-204-708-4	Sequence 4, Appli	c 828	14	2.8	55298	4	US-09-491-356C-1	Sequence 1, Appli
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832	14	2.8	92407	4	US-09-596-002-36	Sequence 36, Appl	905	13	2.6	87	3	US-08-976-413A-93	Sequence 93, Appl
833	14	2.8	99916	4	US-09-816-095-3	Sequence 3, Appl	906	13	2.6	87	5	PCT-US96-06059-93	Sequence 93, Appl
834	14	2.8	112132	4	US-09-741-150-3	Sequence 3, Appl	907	13	2.6	88	4	US-09-523-849-11	Sequence 11, Appl
835	14	2.8	112132	4	US-10-160-187-3	Sequence 3, Appl	908	13	2.6	127	4	US-09-470-276-70	Sequence 70, Appl
836	14	2.8	118067	4	US-09-497-855A-32	Sequence 32, Appl	909	13	2.6	129	1	US-08-664-449-38	Sequence 38, Appl
837	14	2.8	169998	4	US-09-676-610B-24	Sequence 24, Appl	910	13	2.6	137	1	US-08-299-498A-20	Sequence 20, Appl
838	14	2.8	174493	4	US-09-804-471A-3	Sequence 3, Appl	911	13	2.6	137	5	PCT-US95-10813-20	Sequence 20, Appl
839	14	2.8	174493	4	US-10-238-709-3	Sequence 3, Appl	912	13	2.6	159	4	US-09-549-872B-9	Sequence 9, Appl
840	14	2.8	197496	4	US-09-877-177A-10	Sequence 10, Appl	913	13	2.6	159	4	US-09-549-872B-13	Sequence 13, Appl
841	14	2.8	202001	4	US-09-734-674-3	Sequence 3, Appl	914	13	2.6	167	4	US-09-621-976-18057	Sequence 18057, A
842	14	2.8	262223	4	US-09-596-002-41	Sequence 41, Appl	915	13	2.6	169	4	US-09-621-976-10641	Sequence 10641, A
843	14	2.8	319608	4	US-09-539-333D-1	Sequence 1, Appl	916	13	2.6	172	3	US-08-735-545-25	Sequence 25, Appl
844	14	2.8	319608	4	US-09-679-409-1	Sequence 1, Appl	917	13	2.6	172	3	US-09-449-083-25	Sequence 25, Appl
845	14	2.8	392000	4	US-10-027-983-11	Sequence 11, Appl	918	13	2.6	183	4	US-09-134-000C-405	Sequence 405, Appl
846	14	2.8	580073	4	US-08-545-528D-1	Sequence 1, Appl	919	13	2.6	186	4	US-09-134-000C-2912	Sequence 2912, Ap
847	14	2.8	640681	4	US-09-790-988-1	Sequence 1, Appl	920	13	2.6	188	3	US-08-905-124-3	Sequence 3, Appl
848	14	2.8	786431	4	US-09-751-389-3	Sequence 3, Appl	921	13	2.6	192	3	US-09-060-756-505	Sequence 505, App
849	14	2.8	1230025	4	US-09-198-452A-1	Sequence 1, Appl	922	13	2.6	192	4	US-09-670-314-505	Sequence 505, App
850	14	2.8	1664976	4	US-09-916-421B-1	Sequence 1, Appl	923	13	2.6	192	4	US-09-328-352-986	Sequence 986, App
851	13	2.6	15	3	US-08-628-747-26	Sequence 26, Appl	924	13	2.6	194	3	US-08-750-064-7	Sequence 7, Appl
852	13	2.6	17	1	US-08-373-124A-2343	Sequence 2343, Ap	925	13	2.6	204	4	US-09-107-532A-1054	Sequence 1054, Ap
853	13	2.6	17	1	US-08-435-628-2343	Sequence 2343, Ap	926	13	2.6	204	4	US-09-107-532A-1055	Sequence 1055, Ap
854	13	2.6	17	3	US-08-985-162-607	Sequence 607, App	927	13	2.6	207	4	US-09-134-000C-1304	Sequence 1304, Ap
855	13	2.6	17	4	US-09-401-063-607	Sequence 607, App	928	13	2.6	207	4	US-07-670-611-18	Sequence 18, Appl
856	13	2.6	18	2	US-09-156-979-35	Sequence 35, Appl	929	13	2.6	208	1	US-08-220-674-18	Sequence 18, Appl
857	13	2.6	18	4	US-09-387-341-96	Sequence 96, Appl	930	13	2.6	208	1	US-08-445-186-18	Sequence 18, Appl
858	13	2.6	20	4	US-09-360-416-17	Sequence 17, Appl	931	13	2.6	208	1	US-08-446-549-18	Sequence 18, Appl
859	13	2.6	21	4	US-09-422-978-10964	Sequence 10964, A	932	13	2.6	208	2	US-08-446-550-18	Sequence 18, Appl
860	13	2.6	22	1	US-08-742-023-38	Sequence 38, Appl	933	13	2.6	210	4	US-09-313-294A-1617	Sequence 1617, Ap
861	13	2.6	22	3	US-08-968-505-38	Sequence 38, Appl	934	13	2.6	210	4	US-09-134-000C-2299	Sequence 2299, Ap
862	13	2.6	23	3	US-08-991-840A-11	Sequence 11, Appl	935	13	2.6	219	6	5182260-22	Patent No. 5182260
863	13	2.6	29	4	US-09-304-232-394	Sequence 384, App	936	13	2.6	223	6	524792-9	Patent No. 524792
864	13	2.6	30	1	US-08-232-015-44	Sequence 44, Appl	937	13	2.6	224	1	US-08-488-144-3	Sequence 3, Appl
865	13	2.6	30	1	US-08-664-449-19	Sequence 19, Appl	938	13	2.6	224	1	US-09-023-655-736	Sequence 736, Appl
866	13	2.6	36	1	US-08-311-760A-97	Sequence 97, Appl	939	13	2.6	225	4	US-09-313-294A-6099	Sequence 6099, Ap
867	13	2.6	36	2	US-08-774-310-97	Sequence 97, Appl	940	13	2.6	226	6	5182260-1	Patent No. 5182260
868	13	2.6	36	3	US-09-143-776-8	Sequence 8, Appl	941	13	2.6	230	4	US-09-523-849-13	Sequence 13, Appl
869	13	2.6	36	3	US-09-143-776-10	Sequence 10, Appl	942	13	2.6	232	4	US-09-523-849-10	Sequence 10, Appl
870	13	2.6	36	3	US-09-171-025-12	Sequence 12, Appl	943	13	2.6	233	3	US-09-060-756-714	Sequence 714, App
871	13	2.6	36	4	US-08-795-876-28	Sequence 28, Appl	944	13	2.6	233	4	US-09-670-314-714	Sequence 714, App
872	13	2.6	38	1	US-08-373-124A-357	Sequence 357, App	945	13	2.6	233	4	US-09-610-906-3	Sequence 3, Appl
873	13	2.6	38	1	US-08-435-628-357	Sequence 357, App	946	13	2.6	234	4	US-09-252-991A-12427	Sequence 12427, A
874	13	2.6	39	2	US-08-477-553A-35	Sequence 35, Appl	947	13	2.6	239	4	US-09-313-294A-819	Sequence 819, App
875	13	2.6	40	3	US-09-135-639-8	Sequence 8, Appl	948	13	2.6	243	4	US-09-107-532A-132	Sequence 132, App
876	13	2.6	40	3	US-09-135-639-10	Sequence 10, Appl	949	13	2.6	243	4	US-09-523-849-9	Sequence 9, Appl
877	13	2.6	47	4	US-09-641-638-741	Sequence 741, App	950	13	2.6	243	4	US-09-023-655-708	Sequence 708, App
878	13	2.6	47	4	US-09-422-978-1172	Sequence 1172, Ap	951	13	2.6	244	4	US-09-016-434-545	Sequence 545, App
879	13	2.6	50	4	US-08-956-171E-1905	Sequence 1905, Ap	952	13	2.6	249	4	US-09-252-991A-3017	Sequence 3017, Ap
880	13	2.6	51	2	US-08-472-171-23	Sequence 23, Appl	953	13	2.6	251	4	US-09-439-313-348	Sequence 348, App
881	13	2.6	51	2	US-08-472-171-42	Sequence 42, Appl	954	13	2.6	251	4	US-09-352-616A-348	Sequence 348, App
882	13	2.6	51	2	US-08-894-526-23	Sequence 23, Appl	955	13	2.6	251	4	US-09-636-215-348	Sequence 348, App
883	13	2.6	51	2	US-08-894-526-42	Sequence 42, Appl	956	13	2.6	251	4	US-09-685-166A-348	Sequence 348, App
884	13	2.6	51	2	US-09-013-047-23	Sequence 23, Appl	957	13	2.6	252	4	US-09-543-681A-1019	Sequence 1019, Ap
885	13	2.6	51	2	US-09-013-047-23	Sequence 23, Appl	958	13	2.6	252	4	US-09-540-236-1345	Sequence 1345, Ap
886	13	2.6	51	3	US-09-374-597-42	Sequence 42, Appl	959	13	2.6	254	4	US-09-976-594-205	Sequence 205, App
887	13	2.6	51	3	US-09-374-597-42	Sequence 42, Appl	960	13	2.6	258	4	US-09-134-001C-2596	Sequence 2596, Ap
888	13	2.6	52	2	US-08-472-171-28	Sequence 28, Appl	961	13	2.6	258	4	US-09-543-681A-762	Sequence 762, App
889	13	2.6	52	2	US-08-472-171-47	Sequence 47, Appl	962	13	2.6	262	3	US-08-851-362D-8	Sequence 8, Appl
890	13	2.6	52	2	US-08-894-526-28	Sequence 28, Appl	963	13	2.6	262	3	US-09-117-121-21	Sequence 21, Appl
891	13	2.6	52	2	US-08-894-526-47	Sequence 47, Appl	964	13	2.6	264	3	US-08-851-362D-4	Sequence 4, Appl
892	13	2.6	52	2	US-09-013-047-28	Sequence 28, Appl	965	13	2.6	264	3	US-08-851-362D-14	Sequence 14, Appl
893	13	2.6	52	2	US-09-013-047-47	Sequence 47, Appl	966	13	2.6	264	3	US-08-851-362D-14	Sequence 14, Appl
894	13	2.6	52	3	US-09-374-597-28	Sequence 28, Appl	967	13	2.6	264	3	US-08-851-362D-16	Sequence 16, Appl
895	13	2.6	52	3	US-09-374-597-47	Sequence 47, Appl	968	13	2.6	264	3	US-08-851-362D-16	Sequence 16, Appl
896	13	2.6	59	1	US-08-010-099-66	Sequence 66, Appl	969	13	2.6	267	4	US-09-543-681A-3357	Sequence 3357, Ap
897	13	2.6	59	3	US-08-448-716-66	Sequence 66, Appl	970	13	2.6	269	4	US-09-313-294A-3104	Sequence 3104, Ap
898	13	2.6	59	3	US-09-304-186-66	Sequence 66, Appl	971	13	2.6	270	4	US-09-523-849-12	Sequence 12, Appl
899	13	2.6	59	4	US-09-754-532-66	Sequence 66, Appl	972	13	2.6	270	4	US-09-328-352-1083	Sequence 1083, Ap
900	13	2.6	60	3	US-09-145-973-1	Sequence 1, Appl	973	13	2.6	273	4	US-08-313-294A-1745	Sequence 1745, Ap
901	13	2.6	65	1	US-08-664-449-1	Sequence 1, Appl	974	13	2.6	274	3	US-08-905-223-238	Sequence 238, App
902	13	2.6	71	4	US-09-364-539-161	Sequence 161, App	975	13	2.6	274	3	US-08-990-823-72	Sequence 72, Appl
903	13	2.6	87	1	US-08-433-126A-93	Sequence 93, Appl	976	13	2.6	274	4	US-09-610-906-4	Sequence 4, Appl


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;
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Zeller, Karen J.
;   REGISTRATION NUMBER: 37,071
;   REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1813 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: LMODNOT03
;   CLONE: 1574617
; US-09-023-655-407
;
; Query Match          3.4%; Score 17; DB 4; Length 1813;
; Best Local Similarity 100.0%; Pred. No. 25;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 187 GCGAGTGGTGGCAGG 203
;
; Db 289 GCGAGTGGTGGCAGG 305
;
; RESULT 4
; US-09-976-594-941/c
; Sequence 941, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 941
; LENGTH: 7055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 346716.17
; US-09-976-594-941
;
; Query Match          3.4%; Score 17; DB 4; Length 7055;
; Best Local Similarity 100.0%; Pred. No. 24;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 149 CCGAACCCAGCTCTGCA 165
;
; Db 2905 CCGAACCCAGCTCTGCA 2889
;
; RESULT 5
; US-08-961-527-49
; Sequence 49, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
```

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;
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11443 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; US-08-961-527-49
;
; Query Match          3.4%; Score 17; DB 4; Length 11443;
; Best Local Similarity 100.0%; Pred. No. 24;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 327 CTCGATTTCACATGTGA 343
;
; Db 7880 CTCGATTTCACATGTGA 7896
;
; RESULT 6
; US-08-961-527-83/c
; Sequence 83, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
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; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-83

Query Match 3.4%; Score 17; DB 4; Length 28473;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAATAAATA 360
|||||
DB 9319 TTTTTCACAAATAAATA 9303

RESULT 7
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751.389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(786431)
; OTHER INFORMATION: n = A,T,C or G
; US-09-751-389-3

Query Match 3.4%; Score 17; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 TTTTCAATGCTATTTT 348
|||||
DB 159385 TTTTCAATGCTATTTT 159401

RESULT 8
US-09-621-976-13504/c
; Sequence 13504, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13504
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-13504

Query Match 3.2%; Score 16; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 85;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 GAGTGGGTGGCAGGT 204
|||||
DB 55 GAGTGGGTGGCAGGT 40

RESULT 9
US-09-252-991A-4718/c
; Sequence 4718, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4718
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4718

Query Match 3.2%; Score 16; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ACCTGCGCGCGAGGG 184
|||||
DB 174 ACCTGCGCGCGAGGG 159

RESULT 10
US-09-621-976-2247
; Sequence 2247, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2247
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 125..337
; US-09-621-976-2247

Query Match 3.2%; Score 16; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 446 TTCTGAGCTGCTTTGT 461
|||||
DB 181 TTCTGAGCTGCTTTGT 196

RESULT 11
US-09-252-991A-4793
; Sequence 4793, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4793
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4793

Query Match 3.2%; Score 16; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ACCTGCGCGCGAGGG 184
|||||
Db 421 ACCTGCGCGCGAGGG 436

RESULT 12
US-09-252-991A-14857/c
; Sequence 14857, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14857
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14857

Query Match 3.2%; Score 16; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 TCCGGGCACAAAGCTCT 437
|||||
Db 600 TCCGGGCACAAAGCTCT 585

RESULT 13
US-08-969-644-15
; Sequence 15, Application US/08969644
; Patent No. 6096519
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCDT PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,644
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,152
; FILING DATE:
; APPLICATION NUMBER: US/07/661,820
; FILING DATE:
; APPLICATION NUMBER: IT MI 91A000314
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia trachomatis
; STRAIN: GO/86 serotype D (trachoma biovar)
; IMMEDIATE SOURCE:
; CLONE: pUC8-pgo plasmid, ATCC 68314
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..795
US-08-969-644-15

Query Match 3.2%; Score 16; DB 3; Length 795;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAT 359
|||||
Db 617 TTTTTCACAAAAT 632

RESULT 14
US-08-444-189-15
; Sequence 15, Application US/08444189
; Patent No. 6110705
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCDT PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Chlamydia trachomatis
STRAIN: GO/86 serotype D (trachoma biovar)
IMMEDIATE SOURCE:
CLONE: pUC8-pGO plasmid, ATCC 68314
FEATURE:
NAME/KEY: CDS
LOCATION: 1..795
US-08-444-189-15

Query Match 3.2%; Score 16; DB 3; Length 795;
Best Local Similarity 100.0%; Pred.No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAAT 359
|||||
Db 617 TTTTTCACAAAAAT 632

RESULT 15

US-08-468-544-15
Sequence 15, Application US/08468544
Patent No. 6248563
GENERAL INFORMATION:
APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario P.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Chlamydia trachomatis
STRAIN: GO/86 serotype D (trachoma biovar)
IMMEDIATE SOURCE:
CLONE: pUC8-pGO plasmid, ATCC 68314
FEATURE:
NAME/KEY: CDS
LOCATION: 1..795
US-08-468-544-15

Query Match 3.2%; Score 16; DB 3; Length 795;
Best Local Similarity 100.0%; Pred.No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAAT 359
|||||
Db 617 TTTTTCACAAAAAT 632

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	134	26.8	1776	9	US-09-738-626-3211
4	20	4.0	2550	13	US-10-424-599-127200
5	19	3.8	497	10	US-09-918-995-27000
6	19	3.8	15373	15	US-10-311-455-440
7	18	3.6	487	10	US-08-770-961-763
8	18	3.6	512	17	US-10-021-323-16510
9	18	3.6	525	17	US-10-021-323-12895
10	18	3.6	525	17	US-10-021-323-16986
11	18	3.6	544	17	US-10-021-323-16193
12	18	3.6	557	17	US-10-021-323-12806
13	18	3.6	573	17	US-10-021-323-15105
14	18	3.6	578	17	US-10-021-323-13860

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663	13	US-10-027-632-203623	Sequence 203623, A
663	13	US-10-027-632-203624	Sequence 203624, A
663	16	US-10-027-632-203623	Sequence 203623, A
663	16	US-10-027-632-203624	Sequence 203624, A
1823	13	US-10-424-599-44251	Sequence 44251, A
2713	16	US-10-094-749-1396	Sequence 1396, Ap
14006	15	US-10-311-455-1931	Sequence 1931, Ap
3673778	15	US-10-312-841-2	Sequence 2, Appli
119	15	US-10-029-386-22319	Sequence 22319, A
266	13	US-10-424-599-83951	Sequence 83951, A
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430	13	US-10-027-632-314765	Sequence 314765, A
430	15	US-10-198-846-13677	Sequence 13677, A
430	16	US-10-027-632-79451	Sequence 79451, A
430	16	US-10-027-632-314765	Sequence 314765, A
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513	10	US-10-424-599-12216	Sequence 12216, A
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569	9	US-09-864-761-7643	Sequence 7643, Ap
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589	13	US-10-027-632-247553	Sequence 247553, A
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706	13	US-10-027-632-11295	Sequence 11295, A
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743	16	US-10-027-632-110161	Sequence 110161, A
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752	16	US-10-027-632-3263	Sequence 3263, Ap
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C 94	17	3.4	2825	13	US-10-425-114-25100	Sequence 25100, A	C 167	16	3.2	445	11	US-09-864-408A-2861	Sequence 2861, Ap
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C 97	17	3.4	3335	17	US-10-437-963-70024	Sequence 70024, A	C 170	16	3.2	476	17	US-10-021-323-6866	Sequence 6866, Ap
C 98	17	3.4	3729	13	US-10-282-122A-37511	Sequence 37511, A	C 171	16	3.2	476	17	US-10-021-323-6866	Sequence 6866, Ap
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C 104	17	3.4	5771	15	US-10-311-455-1924	Sequence 1924, Ap	C 177	16	3.2	508	13	US-10-027-632-133504	Sequence 133504, A
C 105	17	3.4	7066	10	US-09-919-039-362	Sequence 362, App	C 178	16	3.2	508	13	US-10-027-632-133504	Sequence 133504, A
C 106	17	3.4	9905	15	US-10-311-455-35	Sequence 35, Appl	C 179	16	3.2	528	17	US-10-027-632-133504	Sequence 133504, A
C 107	17	3.4	11443	13	US-10-158-844-49	Sequence 49, Appl	C 180	16	3.2	529	15	US-10-027-632-133504	Sequence 133504, A
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C 109	17	3.4	19553	15	US-10-092-154-1425	Sequence 1425, Ap	C 182	16	3.2	534	17	US-10-021-323-460	Sequence 460, App
C 110	17	3.4	28473	13	US-10-158-844-83	Sequence 83, Appl	C 183	16	3.2	552	15	US-10-029-386-2908	Sequence 2908, Ap
C 111	17	3.4	41540	13	US-10-087-192-721	Sequence 721, App	C 184	16	3.2	552	15	US-10-029-386-2908	Sequence 2908, Ap
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C 115	17	3.4	170245	13	US-10-160-807-4	Sequence 322, App	C 188	16	3.2	565	13	US-10-027-632-133504	Sequence 133504, A
C 116	17	3.4	256493	13	US-10-717-597-322	Sequence 322, App	C 189	16	3.2	565	13	US-10-027-632-133504	Sequence 133504, A
C 117	17	3.4	439892	13	US-10-087-192-1000	Sequence 1000, Ap	C 190	16	3.2	581	17	US-10-437-963-54378	Sequence 54378, A
C 118	17	3.4	786431	15	US-10-087-192-454	Sequence 454, App	C 191	16	3.2	590	13	US-10-425-114-36095	Sequence 36095, A
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C 120	16	3.2	106	9	US-09-969-373-1142	Sequence 1142, Ap	C 193	16	3.2	592	13	US-10-027-632-296727	Sequence 296727, A
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C 123	16	3.2	210	13	US-10-282-122A-5899	Sequence 5899, Ap	C 196	16	3.2	592	16	US-10-027-632-296727	Sequence 296727, A
C 124	16	3.2	210	9	US-09-960-352-14526	Sequence 14526, A	C 197	16	3.2	592	16	US-10-027-632-296727	Sequence 296727, A
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C 127	16	3.2	246	9	US-09-815-242-1398	Sequence 1398, Ap	C 200	16	3.2	603	17	US-10-021-323-12447	Sequence 12447, A
C 128	16	3.2	246	9	US-09-815-242-1408	Sequence 1408, Ap	C 201	16	3.2	603	17	US-10-021-323-12447	Sequence 12447, A
C 129	16	3.2	246	9	US-09-815-242-1460	Sequence 1460, Ap	C 202	16	3.2	603	17	US-10-021-323-12447	Sequence 12447, A
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C 147	16	3.2	351	17	US-10-437-963-11621	Sequence 11621, A	C 220	16	3.2	641	13	US-10-027-632-211687	Sequence 211687, A
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C 153	16	3.2	411	13	US-10-242-535A-43172	Sequence 43172, A	C 226	16	3.2	651	13	US-10-027-632-200912	Sequence 200912, A
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C 243	16	3.2	796	13	US-10-424-599-93951	Sequence 93951, A	316	16	3.2	2196	15	US-10-084-817-120	Sequence 120, App
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C 245	16	3.2	801	16	US-10-027-632-155541	Sequence 155541, A	318	16	3.2	2197	16	US-10-027-632-263096	Sequence 263096, A
C 246	16	3.2	803	13	US-10-027-632-155541	Sequence 155541, A	319	16	3.2	2197	16	US-10-027-632-263097	Sequence 263097, A
C 247	16	3.2	844	9	US-10-425-114-21204	Sequence 21204, A	320	16	3.2	2232	9	US-09-814-353-21193	Sequence 21193, A
C 248	16	3.2	847	13	US-09-909-745-7	Sequence 7, Appl	321	16	3.2	2237	9	US-09-989-920-6	Sequence 6, Appl
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C 252	16	3.2	911	13	US-10-425-114-30217	Sequence 30217, A	325	16	3.2	2340	16	US-09-946-374-286	Sequence 286, App
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C 827	16	3.2	2340	15	US-10-174-569-333	Sequence 333, App	C 900	16	3.2	2340	16	US-10-199-463-333	Sequence 333, App
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C 833	16	3.2	2340	15	US-10-175-743-333	Sequence 333, App	C 906	16	3.2	2340	16	US-10-012-231A-286	Sequence 286, App
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C 841	16	3.2	2340	15	US-10-176-754-333	Sequence 333, App	C 914	16	3.2	2466	17	US-10-437-963-45846	Sequence 45846, A
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C 843	16	3.2	2340	15	US-10-176-759-333	Sequence 333, App	C 916	16	3.2	2580	9	US-09-938-842A-1504	Sequence 1504, App
C 844	16	3.2	2340	15	US-10-176-920-333	Sequence 333, App	C 917	16	3.2	2580	11	US-09-938-842A-1504	Sequence 1504, App
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C 859	16	3.2	2340	15	US-10-176-490-333	Sequence 333, App	C 932	16	3.2	3260	16	US-10-028-248A-210	Sequence 210, App
C 860	16	3.2	2340	15	US-10-176-752-333	Sequence 333, App	C 933	16	3.2	3260	17	US-10-107-782-210	Sequence 210, App
C 861	16	3.2	2340	15	US-10-176-981-333	Sequence 333, App	C 934	16	3.2	3660	17	US-10-221-596B-13	Sequence 13, Appl
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C 865	16	3.2	2340	15	US-10-179-521-333	Sequence 333, App	C 938	16	3.2	4111	13	US-10-257-021-146	Sequence 146, App
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C 867	16	3.2	2340	15	US-10-012-064A-286	Sequence 286, App	C 940	16	3.2	4137	14	US-10-052-664-2	Sequence 2, Appli
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C 884	16	3.2	2340	15	US-10-013-906A-286	Sequence 286, App	C 957	16	3.2	6478	15	US-10-240-453-143	Sequence 143, App
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Sequence 1342, Ap
Sequence 465, App

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16 3.2 78072 16 US-10-085-117-154
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16 3.2 92076 17 US-10-322-281-465

ALIGNMENTS

RESULT 1
US-09-987-763-7
; Sequence 7, Application US/09987763
; Publication No. US20030017553A1
; GENERAL INFORMATION:
; APPLICANT: Rayapati, P. John
; APPLICANT: Crafton, Corey M.
; TITLE OF INVENTION: Nucleotide Sequences for Transcriptional Regulation in
; TITLE OF INVENTION: Corynebacterium glutamicum
; FILE REFERENCE: 1533.1940002
; CURRENT APPLICATION NUMBER: US/09/987,763
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,219
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-987-763-7

Query Match 100.0%; Score 500; DB 13; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.1e-268;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAACAGCCAGGTTAGCGGTGTAACCCACGAGTTCGGCAACATGACGGCGAGAGA 60
Db 1 AAAACAGCCAGGTTAGCGGTGTAACCCACGAGTTCGGCAACATGACGGCGAGAGA 60
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61 GCCCACCACATTCGGATTTCCGCTCCGATAAAGCCAGCGCCCATATTTTCAGGAGGATT 120
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481 ATCAGGAAGTGGGATCGAAA 500
481 ATCAGGAAGTGGGATCGAAA 500

RESULT 2
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIRO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 55.0%; Score 275; DB 9; Length 3309400;
Best Local Similarity 99.2%; Pred. No. 1.7e-142;
Matches 475; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy	202	GGTTTTAGTCGGGTTTTAAGCGTTGCCAGGCGGAGTGGTGAGCAAGACGCTAGCTTGGGG	261
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Qy	262	AGCGAACCATTATTTAGTCACTTTGGCAGAGCAGTGCACAAATTCGACGGGCATAGATTGG	321
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Qy	322	TTTTTGCTCGATTTACAAATGTATTTTTTCAACAAAATAATCACTTCGCTCGACCACATTT	381
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Qy	382	TCGGACATAATCCGGGCATAATTAAAGGTGTAAACAAAGGAATCCGGGCACAAGCTCTTGCT	441
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Qy	442	GATTTTCTGAGCTGCTTTGTGGTTGTTCGGTTGTAGGAAATCAGGAAGTGGGATCGAAA	500
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Db      131  CGGATCCCGGAAC 118

RESULT 4
US-10-424-599-127200/c
; Sequence 127200, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 127200
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85868C.1
US-10-424-599-127200

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	Query Match	26.8%	Score 134	DB 9	Length 1776
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QY	82	GCTCGATAAGCCAGCGCCCATATTTCAGGAGGAGATTTCGCTGGGTTTGGCGACATT	141		
Db	191	GCTCGATAAAGCCAGCGCCCATATTTCAGGAGGAGATTTCGCTGGGTTTGGCGACATT	132		

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US-10-311-455-440/c
; Sequence 440, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Sequence of Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 440
; LENGTH: 15373
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-440

Query Match      3.8%; Score 19; DB 15; Length 15373;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      344 TTTTTCACACAAAATAAC 362
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RESULT 7
US-09-770-961-763
; Sequence 763, Application US/09770961
; Publication No. US20030115639A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2026 (PAPA-015PRV)
; CURRENT APPLICATION NUMBER: US/09/770,961
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,466
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-09-770-961-763
; Sequence 12895, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 12895
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-007-Q6-N6-E3
; US-10-021-323-12895

Query Match      3.6%; Score 18; DB 17; Length 512;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      473 TTAGGAAATCAGGAAGT 490
Db      388 TTAGGAAATCAGGAAGT 371

RESULT 9
US-10-021-323-12895/c
; Sequence 12895, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 12895
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-007-Q6-N6-E3
; US-10-021-323-12895

Query Match      3.6%; Score 18; DB 17; Length 525;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      430 CAAGCTCTTGCTGATTTT 447
Db      467 CAAGCTCTTGCTGATTTT 484

RESULT 8
US-10-021-323-16510/c
; Sequence 16510, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16510
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-020-Q6-N6-D3
; US-10-021-323-16510

Query Match      3.6%; Score 18; DB 17; Length 512;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      473 TTAGGAAATCAGGAAGT 490
Db      388 TTAGGAAATCAGGAAGT 371

RESULT 9
US-10-021-323-12895/c
; Sequence 12895, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 12895
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-007-Q6-N6-E3
; US-10-021-323-12895

Query Match      3.6%; Score 18; DB 17; Length 525;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      430 CAAGCTCTTGCTGATTTT 447
Db      467 CAAGCTCTTGCTGATTTT 484

```

QY 473 TTAGGGAATCAGGAAGT 490
|||||
Db 421 TTAGGGAATCAGGAAGT 404

RESULT 10

US-10-021-323-16986/c
; Sequence 16986, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16986
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; LOCATION: (1)..(557)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-026-Q6-N6-E2
US-10-021-323-16986

Query Match 3.6%; Score 18; DB 17; Length 525;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGGAATCAGGAAGT 490
|||||
Db 430 TTAGGGAATCAGGAAGT 413

RESULT 11

US-10-021-323-16193/c
; Sequence 16193, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16193
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-015-Q1-N6-G5
US-10-021-323-16193

Query Match 3.6%; Score 18; DB 17; Length 544;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGGAATCAGGAAGT 490
|||||
Db 406 TTAGGGAATCAGGAAGT 389

RESULT 12

US-10-021-323-12806
; Sequence 12806, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 12806
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(557)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-007-Q6-K6-E3
US-10-021-323-12806

Query Match 3.6%; Score 18; DB 17; Length 557;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGGAATCAGGAAGT 490
|||||
Db 132 TTAGGGAATCAGGAAGT 149

RESULT 13

US-10-021-323-15105
; Sequence 15105, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 15105
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-020-Q6-K6-D3
US-10-021-323-15105

Query Match 3.6%; Score 18; DB 17; Length 573;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGGAATCAGGAAGT 490
|||||
Db 207 TTAGGGAATCAGGAAGT 224

RESULT 14

US-10-021-323-13860
; Sequence 13860, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 13860
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(578)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-015-Q1-K6-G5
US-10-021-323-13860

Query Match 3.6%; Score 18; DB 17; Length 578;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGGAATCAGGAAGT 490
Db 197 TTAGGGAATCAGGAAGT 214

RESULT 15
US-09-918-995-12576/c
; Sequence 12576, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12576
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(584)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-12576

Query Match 3.6%; Score 18; DB 10; Length 584;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 TTCTGCAGGCGCATAGATT 319
Db 475 TTCTGCAGGCGCATAGATT 458

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 14:18:07 ; Search time 2385 Seconds
(without alignments)
6260.415 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagggc.....atcagggaagtggaagcgaag 500

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	4.2	801	29	CC529519 CH240 405
2	21	4.2	973	13	BUS19692 AGENCOURT
3	20	4.0	213	29	CE545692 tigr-gss-
4	20	4.0	346	28	AQ959051 LEREG96TR

C	5	20	4.0	360	14	CA912211	PCS02658
C	6	20	4.0	393	12	BM892066	Sam47H05.
C	7	20	4.0	490	9	AU203244	AU203244
C	8	20	4.0	539	9	AV960301	AV960301
C	9	20	4.0	541	13	BM204471	BM204471
C	10	20	4.0	551	12	BM521341	BM521341
C	11	20	4.0	557	12	BI944599	BI944599
C	12	20	4.0	570	13	BM277800	BM277800
C	13	20	4.0	574	13	BQ296476	BQ296476
C	14	20	4.0	577	12	BI943495	BI943495
C	15	20	4.0	581	28	AZ493804	AZ493804
C	16	20	4.0	587	10	BE805810	BE805810
C	17	20	4.0	590	10	AW759418	AW759418
C	18	20	4.0	614	12	BJ110320	BJ110320
C	19	20	4.0	616	12	BJ110370	BJ110370
C	20	20	4.0	617	10	AW279214	AW279214
C	21	20	4.0	621	9	AU207364	AU207364
C	22	20	4.0	633	28	AZ869794	AZ869794
C	23	20	4.0	655	13	BM216978	BM216978
C	24	20	4.0	673	14	CF243553	CF243553
C	25	20	4.0	689	14	CF806395	CF806395
C	26	20	4.0	698	13	BM214172	BM214172
C	27	20	4.0	727	12	BP014381	BP014381
C	28	20	4.0	788	28	BH729346	BH729346
C	29	20	4.0	843	14	CK250567	CK250567
C	30	20	4.0	915	14	CK258134	CK258134
C	31	20	4.0	920	14	CK254139	CK254139
C	32	20	4.0	922	14	CK258904	CK258904
C	33	20	4.0	945	28	AZ166685	AZ166685
C	34	20	4.0	974	14	CK251495	CK251495
C	35	20	4.0	978	14	CK254992	CK254992
C	36	20	4.0	1006	14	CK250376	CK250376
C	37	20	4.0	1167	28	CC268378	CC268378
C	38	19	3.8	343	14	CD673749	CD673749
C	39	19	3.8	386	14	R73793	R73793
C	40	19	3.8	430	14	H29150	H29150
C	41	19	3.8	447	14	T09037	T09037
C	42	19	3.8	454	10	BF713406	BF713406
C	43	19	3.8	461	14	CB736812	CB736812
C	44	19	3.8	482	9	AU231249	AU231249
C	45	19	3.8	515	13	BQ856912	BQ856912
C	46	19	3.8	521	10	BE252127	BE252127
C	47	19	3.8	521	28	BZ675425	BZ675425
C	48	19	3.8	549	29	CE284696	CE284696
C	49	19	3.8	559	28	BH044780	BH044780
C	50	19	3.8	590	12	BM722923	BM722923
C	51	19	3.8	592	12	BJ434874	BJ434874
C	52	19	3.8	620	28	AZ634145	AZ634145
C	53	19	3.8	637	29	CC749924	CC749924
C	54	19	3.8	638	12	BM706879	BM706879
C	55	19	3.8	640	29	CE257551	CE257551
C	56	19	3.8	649	13	BQ578571	BQ578571
C	57	19	3.8	653	10	BE255492	BE255492
C	58	19	3.8	676	9	AI584574	AI584574
C	59	19	3.8	689	10	BB375011	BB375011
C	60	19	3.8	717	28	BZ415107	BZ415107
C	61	19	3.8	756	9	AI721333	AI721333
C	62	19	3.8	759	29	CE079578	CE079578
C	63	19	3.8	768	12	BG110902	BG110902
C	64	19	3.8	789	28	BZ419232	BZ419232
C	65	19	3.8	828	28	BH430252	BH430252
C	66	19	3.8	829	28	BH706484	BH706484
C	67	19	3.8	830	28	BZ638567	BZ638567
C	68	19	3.8	859	28	BH422618	BH422618
C	69	19	3.8	862	28	BZ788270	BZ788270
C	70	19	3.8	862	29	CG049916	CG049916
C	71	19	3.8	876	12	BG192528	BG192528
C	72	19	3.8	877	29	CG971007	CG971007
C	73	19	3.8	880	28	CC404611	CC404611
C	74	19	3.8	893	29	CG127404	CG127404
C	75	19	3.8	899	13	BU508902	BU508902
C	76	19	3.8	910	10	BE894163	BE894163
C	77	19	3.8	919	28	CC390023	CC390023

C 78	19	3.8	924	29	CG947826	CG947826 MBEJC65TF	151	18	3.6	638	28	AZ406401	AZ406401 LM0175D12
C 79	19	3.8	934	29	CNS01KHU	AL1148355 Anopheles	C 152	18	3.6	646	29	CE841301	CE841301 tigr-gss-
C 80	19	3.8	939	29	CG304202	CG304202 CGXCZ66TH	153	18	3.6	648	12	BJ543393	BJ543393 BJ543393
C 81	19	3.8	940	29	CG366263	CG366263 PUHNT31TD	154	18	3.6	657	13	EX301727	EX301727 BX301727
C 82	19	3.8	955	29	CG026168	CG026168 ZMMBC056	C 155	18	3.6	679	13	BW009367	BW009367 BW009367
C 83	19	3.8	988	12	BM474134	BM474134 AGENCOURT	C 156	18	3.6	681	13	BO402195	BO402195 GA_EB004
C 84	19	3.8	1233	11	BM546655	BM546655 AGENCOURT	C 157	18	3.6	687	14	CF325795	CF325795 PLaJXT002
C 85	19	3.8	2057	11	AK081795	AK081795 Mus muscu	C 158	18	3.6	689	28	BH999275	BH999275 oeh12c03
C 86	18	3.6	112	12	BJ365130	BJ365130 BJ365130	C 159	18	3.6	692	13	CA063584	CA063584 ssaalr050
C 87	18	3.6	115	12	BJ365299	BJ365299 BJ365299	C 160	18	3.6	695	12	BI548831	BI548831 603196945
C 88	18	3.6	129	12	BJ370960	BJ370960 BJ370960	C 161	18	3.6	699	13	BY709232	BY709232 BY709232
C 89	18	3.6	133	12	BJ392064	BJ392064 BJ392064	C 162	18	3.6	706	28	BH842871	BH842871 TC3-55J13
C 90	18	3.6	142	12	BP522231	BP522231 BP522231	163	18	3.6	710	29	AG101703	AG101703 Pan trogl
C 91	18	3.6	150	12	BJ396709	BJ396709 BJ396709	164	18	3.6	715	28	BH950483	BH950483 oeh79h06
C 92	18	3.6	204	28	BZ149860	BZ149860 CH230-359	165	18	3.6	719	13	BY764464	BY764464 BY764464
C 93	18	3.6	205	13	EX680967	EX680967 EX680967	C 166	18	3.6	722	14	CK247466	CK247466 EST731103
C 94	18	3.6	242	9	AV341489	AV341489 AV341489	C 167	18	3.6	728	10	BE292438	BE292438 601057773
C 95	18	3.6	266	28	BH192601	BH192601 TC3-1C12	C 168	18	3.6	731	28	BH968929	BH968929 odj05h11
C 96	18	3.6	274	10	BB496689	BB496689 BB496689	C 169	18	3.6	737	28	BH794283	BH794283 ME MBA000
C 97	18	3.6	286	10	BF713653	BF713653 ESTPBL200	170	18	3.6	738	14	CK266718	CK266718 EST712796
C 98	18	3.6	298	10	BE103413	BE103413 UI-R-BX0-	C 171	18	3.6	742	12	BI757516	BI757516 603029665
C 99	18	3.6	319	29	CG798404	CG798404 SALK 1462	C 172	18	3.6	749	29	CE838709	CE838709 tigr-gss-
C 100	18	3.6	335	9	AI396114	AI396114 487011F09	C 173	18	3.6	758	29	EX211946	EX211946 Dario rer
C 101	18	3.6	335	12	BI741865	BI741865 kt61h12.Y	C 174	18	3.6	766	28	BH211256	BH211256 Sm1-54G6
C 102	18	3.6	363	9	AA825471	AA825471 od04b04.s	C 175	18	3.6	768	13	BU707899	BU707899 UI-M-FR0-
C 103	18	3.6	365	10	BE045085	BE045085 hm28c02.x	C 176	18	3.6	773	13	BU199494	BU199494 603949455
C 104	18	3.6	372	28	AQ045467	AQ045467 RPI111-36	C 177	18	3.6	791	29	CG109823	CG109823 PUFN185TD
C 105	18	3.6	379	13	EX502009	EX502009 DKFZP779F	C 178	18	3.6	794	12	BI549285	BI549285 603189923
C 106	18	3.6	395	12	BG301443	BG301443 kt01c01.Y	C 179	18	3.6	795	29	CG487994	CG487994 CH240-319
C 107	18	3.6	396	12	BG301652	BG301652 kt03g09.Y	C 180	18	3.6	802	28	BZ401265	BZ401265 EINH585TR
C 108	18	3.6	411	9	AI549192	AI549192 UI-R-C3-t	C 181	18	3.6	803	12	BI912821	BI912821 603176013
C 109	18	3.6	414	9	AI825477	AI825477 wb73d06.x	C 182	18	3.6	808	12	EG445766	EG445766 GA_EB002
C 110	18	3.6	431	29	CG860561	CG860561 NDL-26M6	C 183	18	3.6	810	12	EG114422	EG114422 602285715
C 111	18	3.6	458	10	BF224006	BF224006 7q36f06.x	C 184	18	3.6	810	12	BH645807	BH645807 BOHTR35TR
C 112	18	3.6	472	28	BH844363	BH844363 TC3-55J14	185	18	3.6	815	12	BI192846	BI192846 602945219
C 113	18	3.6	473	12	BG347817	BG347817 dac80d12.x	C 186	18	3.6	820	28	CC067387	CC067387 CSU-K33r
C 114	18	3.6	493	10	BF059589	BF059589 7k63b12.x	C 187	18	3.6	828	28	EX213922	EX213922 Dario rer
C 115	18	3.6	493	28	AZ924819	AZ924819 4906.1d55	188	18	3.6	831	28	BZ389182	BZ389182 EIND160TF
C 116	18	3.6	505	14	CD542321	CD542321 B0238E12-	189	18	3.6	831	29	BZ399886	BZ399886 EINH848TR
C 117	18	3.6	526	14	CD542568	CD542568 B0242A02-	190	18	3.6	831	29	CG112105	CG112105 FUGGH38TB
C 118	18	3.6	530	13	BK301726	BK301726 BX301726	191	18	3.6	840	28	BZ393980	BZ393980 EINHAD26TR
C 119	18	3.6	531	12	BP522327	BP522327 BP522327	192	18	3.6	850	28	AZ674369	AZ674369 ENTMA52TR
C 120	18	3.6	541	10	BF266205	BF266205 HV_CEA001	193	18	3.6	852	13	BQ509370	BQ509370 EST616785
C 121	18	3.6	544	28	BH195592	BH195592 TC3-4E3.T	194	18	3.6	860	12	BI768310	BI768310 603053608
C 122	18	3.6	551	14	CD525790	CD525790 kw26a10.Y	C 195	18	3.6	862	12	BG474093	BG474093 GA_EB004
C 123	18	3.6	562	9	AV553806	AV553806 AV553806	C 196	18	3.6	873	28	BH155174	BH155174 ENTRW45TF
C 124	18	3.6	565	14	CF202319	CF202319 RR890915N	C 197	18	3.6	874	10	BF279440	BF279440 GA_EB004
C 125	18	3.6	568	13	BQ738972	BQ738972 PC38912.Y	C 198	18	3.6	875	14	CK252826	CK252826 EST736463
C 126	18	3.6	570	13	BQ692111	BQ692111 pt03a08.Y	C 199	18	3.6	879	29	CG769256	CG769256 TCB47.2.C
C 127	18	3.6	573	10	BQ053511	BQ053511 GA_Ea002	C 200	18	3.6	886	13	BU956652	BU956652 AGENCOURT
C 128	18	3.6	573	13	BQ408123	BQ408123 GA_Ed000	C 201	18	3.6	889	28	AZ674182	AZ674182 ENTLV82TR
C 129	18	3.6	573	13	BQ408124	BQ408124 GA_Ed000	C 202	18	3.6	892	29	CG976368	CG976368 MBEHD01TF
C 130	18	3.6	575	9	AU236000	AU236000 AU236000	C 203	18	3.6	894	28	CC066598	CC066598 CSU-K33r
C 131	18	3.6	575	10	AW616607	AW616607 EST233018	C 204	18	3.6	900	13	BX342290	BX342290 BX342290
C 132	18	3.6	577	28	AQ518331	AQ518331 HS_5102.B	C 205	18	3.6	904	13	BU159221	BU159221 AGENCOURT
C 133	18	3.6	594	10	BE055030	BE055030 GA_Ea001	C 206	18	3.6	918	28	CC078983	CC078983 CSU-K33r
C 134	18	3.6	595	14	BQ405675	BQ405675 GA_Ed008	C 207	18	3.6	925	13	BQ223735	BQ223735 AGENCOURT
C 135	18	3.6	595	14	CF107618	CF107618 Shult-zomi	C 208	18	3.6	927	29	BH157874	BH157874 ENTSQ81TR
C 136	18	3.6	597	12	BG445288	BG445288 GA_Ea002	C 209	18	3.6	927	29	CG650230	CG650230 OGVC004TH
C 137	18	3.6	600	13	BQ603343	BQ603343 MI-P-NA-a	C 210	18	3.6	932	28	BZ680565	BZ680565 PUBFN06TD
C 138	18	3.6	606	29	CE574126	CE574126 tigr-gss-	C 211	18	3.6	948	10	BF168433	BF168433 601776024
C 139	18	3.6	607	13	BQ415092	BQ415092 GA_Ed009	C 212	18	3.6	984	28	CC299564	CC299564 CH261-67J
C 140	18	3.6	611	28	BZ393490	BZ393490 EINHBB5TF	C 213	18	3.6	986	12	BG334996	BG334996 602403436
C 141	18	3.6	613	28	AQ262931	AQ262931 CITBI-E1	C 214	18	3.6	995	29	CG650238	CG650238 OGVC004TV
C 142	18	3.6	622	12	BM988514	BM988514 UI-H-DHO-	C 215	18	3.6	999	10	BE454301	BE454301 AGENCOURT
C 143	18	3.6	622	29	CE028049	CE028049 tigr-gss-	C 216	18	3.6	1005	12	BM454001	BM454001 603021162
C 144	18	3.6	624	13	CD486484	CD486484 CRH3-ID11	C 217	18	3.6	1012	12	BI488630	BI488630 602268538
C 145	18	3.6	628	13	BQ402196	BQ402196 GA_Ed004	C 218	18	3.6	1071	10	BF964867	BF964867 602268538
C 146	18	3.6	628	28	BH649701	BH649701 BOMEL51TF	C 219	18	3.6	1100	29	CNS04255	CNS04255 Teltraodon
C 147	18	3.6	630	13	BQ413831	BQ413831 GA_Ed007	C 220	18	3.6	1120	28	CC292953	CC292953 CH261-130
C 148	18	3.6	631	13	EX680735	EX680735 BX680735	C 221	18	3.6	1479	28	CC324015	CC324015 TAM32-16A
C 149	18	3.6	633	14	CD813917	CD813917 EN15_02IG	C 222	18	3.6	2687	11	BC042192	BC042192 Homo sapi
C 150	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 223	18	3.6				

C 224	18	3-6	2688	11	BC030284	BC030284 Homo sapi	C 297	17	3-4	382	29	CG021490
C 225	18	3-6	3396	11	AK089442	AK089442 Mus muscu	C 298	17	3-4	383	12	BG9900748
C 226	17	3-4	56	29	BX209742	BX209742 Danio rer	C 299	17	3-4	383	13	BY372025
C 227	17	3-4	94	9	AA503707	AA503707 ns50d12.s	C 300	17	3-4	387	11	CNS093RS
C 228	17	3-4	146	9	AI006254	AI006254 ua88g04.r	C 301	17	3-4	389	12	BJ140510
C 229	17	3-4	197	12	BI007827	BI007827 QV3-RT007	C 302	17	3-4	389	12	BJ183744
C 230	17	3-4	204	13	BW170281	BW170281 BW170281	C 303	17	3-4	392	9	AA197676
C 231	17	3-4	204	28	AQ974424	AQ974424 RPCI-23-3	C 304	17	3-4	396	28	AA0870729
C 232	17	3-4	218	29	CE498075	CE498075 tigr-gss-	C 305	17	3-4	396	28	AG241274
C 233	17	3-4	221	29	BX204239	BX204239 Danio rer	C 306	17	3-4	398	29	CE384478
C 234	17	3-4	236	10	BB301122	BB301122 BB301122	C 307	17	3-4	399	9	AA139630
C 235	17	3-4	236	28	AZ379779	AZ379779 IM013511	C 308	17	3-4	407	10	AW164159
C 236	17	3-4	239	12	BM418295	BM418295 952013H01	C 309	17	3-4	408	29	AG029027
C 237	17	3-4	240	10	BB170277	BB170277 BB170277	C 310	17	3-4	409	12	BJ200918
C 238	17	3-4	240	13	C31037	C31037 C31037 Yyji	C 311	17	3-4	409	28	BZ305623
C 239	17	3-4	240	13	C58876	C58876 C58876 Yyji	C 312	17	3-4	410	10	BE247755
C 240	17	3-4	244	14	H34292	H34292 ES111070.R	C 313	17	3-4	412	13	B0430303
C 241	17	3-4	248	13	BR300139	BR300139 BR300139	C 314	17	3-4	413	28	AQ528831
C 242	17	3-4	255	14	W89747	W89747 mf75d03.r1	C 315	17	3-4	417	29	BX197777
C 243	17	3-4	264	10	BE022146	BE022146 sm68a10.Y	C 316	17	3-4	420	13	BX480118
C 244	17	3-4	267	10	BB372134	BB372134 BB372134	C 317	17	3-4	421	28	CC160358
C 245	17	3-4	268	9	AV134545	AV134545 AV134545	C 318	17	3-4	424	14	CF349992
C 246	17	3-4	268	14	CB945859	CB945859 AGENCOURT	C 319	17	3-4	425	10	AW894114
C 247	17	3-4	271	10	BB576952	BB576952 BB576952	C 320	17	3-4	425	28	AZ919276
C 248	17	3-4	275	10	BB195768	BB195768 BB195768	C 321	17	3-4	427	9	AI889498
C 249	17	3-4	278	10	BB552429	BB552429 BB552429	C 322	17	3-4	430	10	BF990273
C 250	17	3-4	279	10	BB455278	BB455278 BB455278	C 323	17	3-4	430	29	CC870478
C 251	17	3-4	284	28	BZ956930	BZ956930 PGH005E10	C 324	17	3-4	433	9	AA000841
C 252	17	3-4	287	10	BB400137	BB400137 BB400137	C 325	17	3-4	436	12	BG240668
C 253	17	3-4	289	10	BB022169	BB022169 BB022169	C 326	17	3-4	436	28	BH4433508
C 254	17	3-4	295	10	BB4547695	BB4547695 BB4547695	C 327	17	3-4	437	12	BG518032
C 255	17	3-4	295	28	AZ261437	AZ261437 RPCI-23-4	C 328	17	3-4	442	13	BQ207915
C 256	17	3-4	298	14	D71093	D71093 CELK062A4R	C 329	17	3-4	443	12	BJ196388
C 257	17	3-4	299	10	BB179024	BB179024 BB179024	C 330	17	3-4	443	13	BQ423126
C 258	17	3-4	300	9	AV118395	AV118395 AV118395	C 331	17	3-4	446	10	BF284630
C 259	17	3-4	300	9	AV179873	AV179873 AV179873	C 332	17	3-4	446	12	BI662660
C 260	17	3-4	300	9	AV180188	AV180188 AV180188	C 333	17	3-4	450	9	AL589262
C 261	17	3-4	300	9	AV180416	AV180416 AV180416	C 334	17	3-4	451	10	BE556224
C 262	17	3-4	300	9	AV182745	AV182745 AV182745	C 335	17	3-4	451	14	W95278
C 263	17	3-4	300	10	BB190034	BB190034 BB190034	C 336	17	3-4	452	10	BE556224
C 264	17	3-4	300	13	C31586	C31586 C31586 Yyji	C 337	17	3-4	453	12	BI425240
C 265	17	3-4	300	13	C32629	C32629 C32629 Yyji	C 338	17	3-4	454	12	BG346646
C 266	17	3-4	300	13	C33146	C33146 C33146 Yyji	C 339	17	3-4	455	13	B0851558
C 267	17	3-4	302	13	B0429125	B0429125 UI-HF-BNO	C 340	17	3-4	455	28	AQ598793
C 268	17	3-4	304	10	BB188452	BB188452 BB188452	C 341	17	3-4	458	13	BY152165
C 269	17	3-4	309	9	AA144291	AA144291 mr80c04.r	C 342	17	3-4	458	13	BQ523668
C 270	17	3-4	309	9	AI822384	AI822384 I0-837T3	C 343	17	3-4	461	28	AZ839742
C 271	17	3-4	310	9	AA379007	AA379007 EST91773	C 344	17	3-4	462	29	DR5B9T
C 272	17	3-4	312	28	CC045458	CC045458 3591.1.17	C 345	17	3-4	464	9	AA722948
C 273	17	3-4	313	10	BB266286	BB266286 BB266286	C 346	17	3-4	466	10	AW504614
C 274	17	3-4	317	13	C96591	C96591 C96591 Marc	C 347	17	3-4	466	9	AI172393
C 275	17	3-4	318	9	AA093687	AA093687 cl0573.re	C 348	17	3-4	469	10	BE332853
C 276	17	3-4	322	9	AI850687	AI850687 UI-M-BG1-	C 349	17	3-4	470	9	AI645119
C 277	17	3-4	322	9	AU710680	AU710680 AU210680	C 350	17	3-4	470	9	AA497449
C 278	17	3-4	325	9	AA4769952	AA4769952 aa74f03.s	C 351	17	3-4	471	9	AI645840
C 279	17	3-4	325	9	AA457593	AA457593 aa89a02.r	C 352	17	3-4	473	28	BZ364163
C 280	17	3-4	328	9	AA062436	AA062436 CM0-CT004	C 353	17	3-4	473	28	BZ622502
C 281	17	3-4	334	9	AA631891	AA631891 np69c11.s	C 354	17	3-4	476	13	B0040380
C 282	17	3-4	338	9	AI299785	AI299785 gn09a12.x	C 355	17	3-4	479	29	CE032418
C 283	17	3-4	340	12	BG346574	BG346574 daa38d12.	C 356	17	3-4	480	14	CB386468
C 284	17	3-4	341	28	AQ453345	AQ453345 LMAJFV1.1	C 357	17	3-4	483	28	AQ857789
C 285	17	3-4	342	9	AI505804	AI505804 vi43a03.x	C 358	17	3-4	485	29	CE623590
C 286	17	3-4	350	9	AU044475	AU044475 AU044475	C 359	17	3-4	486	9	AI029460
C 287	17	3-4	351	13	BU020153	BU020153 QHE26J01.	C 360	17	3-4	487	12	BM276840
C 288	17	3-4	356	10	AW545012	AW545012 C0188F02-	C 361	17	3-4	487	13	BX517845
C 289	17	3-4	357	28	BH884533	BH884533 hw52e11.g	C 362	17	3-4	488	28	BZ252606
C 290	17	3-4	362	29	LEWFD15	BX530447 Leishmani	C 363	17	3-4	491	9	AA144528
C 291	17	3-4	363	13	BY415455	BY415455 BY415455	C 364	17	3-4	493	14	CB642978
C 292	17	3-4	365	9	AI851326	AI851326 UI-M-BH0-	C 365	17	3-4	495	12	BM970188
C 293	17	3-4	372	28	AZ720459	AZ720459 RPCI-24-1	C 366	17	3-4	496	28	AZ920560
C 294	17	3-4	377	14	H08903	H08903 Y188608.r1	C 367	17	3-4	497	11	CNS09DJH
C 295	17	3-4	382	10	AW503403	AW503403 UI-HF-BNO	C 368	17	3-4	502	10	BE235625
C 296	17	3-4	382	28	AZ596568	AZ596568 1M0409J22	C 369	17	3-4	502	14	CA507675

370	17	3.4	503	10	BE234827	142076 MA	443	17	3.4	611	28	BZ396350
371	17	3.4	508	28	BH205806	Sm1-59K21	444	17	3.4	612	13	BU720472
372	17	3.4	509	28	BZ366237	ic95e11.b	445	17	3.4	613	10	AW958341
373	17	3.4	511	10	BE949917	UT-M-CD0-	446	17	3.4	614	14	CB826216
374	17	3.4	512	10	BF547971	UT-R-E0-b	447	17	3.4	614	14	CF108178
375	17	3.4	514	28	CS167021	1157904.b	448	17	3.4	614	29	DR41D5T
376	17	3.4	515	13	CF631501	BU430482	449	17	3.4	615	13	BU046390
377	17	3.4	516	14	CF631501	zmrw848_0	450	17	3.4	615	29	AG034990
378	17	3.4	519	10	BQ019901	BP019901	451	17	3.4	616	9	AL777133
379	17	3.4	523	13	BQ296182	8an87h03	452	17	3.4	616	14	CD995047
380	17	3.4	525	13	BX529099	EX529099	453	17	3.4	616	28	AQ504602
381	17	3.4	525	14	CA951631	CA951631	454	17	3.4	617	12	BI713471
382	17	3.4	528	10	BE017207	BE017207	455	17	3.4	619	29	CE220286
383	17	3.4	529	10	BE336122	u85e06.Y	456	17	3.4	620	12	BI943651
384	17	3.4	529	28	AZ635626	AZ635626	457	17	3.4	622	12	BM719104
385	17	3.4	531	12	BU144969	BU144969	458	17	3.4	622	13	BU304458
386	17	3.4	532	10	BF921494	BF921494	459	17	3.4	625	13	CA041174
387	17	3.4	532	10	BF346572	BF346572	460	17	3.4	627	29	CE413548
388	17	3.4	533	10	BF959478	BF959478	461	17	3.4	628	28	AZ861189
389	17	3.4	539	9	AU040106	AU040106	462	17	3.4	630	11	CNS09DUJ
390	17	3.4	539	28	BZ677400	BZ677400	463	17	3.4	630	13	BU720459
391	17	3.4	540	28	CE160415	CE160415	464	17	3.4	632	13	BX265897
392	17	3.4	541	10	BG007940	BG007940	465	17	3.4	632	14	CD074694
393	17	3.4	541	14	CD721977	CD721977	466	17	3.4	632	13	BU624766
394	17	3.4	543	29	CG582279	CG582279	467	17	3.4	633	13	BQ110879
395	17	3.4	545	14	CA892793	CA892793	468	17	3.4	636	28	BZ317309
396	17	3.4	546	10	AW500273	AW500273	469	17	3.4	636	28	BZ317309
397	17	3.4	547	28	AQ793036	AQ793036	470	17	3.4	637	13	BQ344665
398	17	3.4	550	9	AV719416	AV719416	471	17	3.4	638	13	BX265896
399	17	3.4	552	13	BU288458	BU288458	472	17	3.4	638	28	AQ247896
400	17	3.4	555	14	CF138280	CF138280	473	17	3.4	639	10	AW551711
401	17	3.4	558	29	CE636215	CE636215	474	17	3.4	641	12	BG573770
402	17	3.4	559	10	BE813907	BE813907	475	17	3.4	641	13	BU287460
403	17	3.4	561	28	AQ710202	AQ710202	476	17	3.4	642	13	BU289975
404	17	3.4	564	28	BZ395340	BZ395340	477	17	3.4	642	28	BZ415530
405	17	3.4	570	29	CE082576	CE082576	478	17	3.4	643	29	CG066082
406	17	3.4	570	29	CG980089	CG980089	479	17	3.4	645	28	BZ339796
407	17	3.4	571	28	BH777894	BH777894	480	17	3.4	645	28	BZ339796
408	17	3.4	572	28	BZ817270	BZ817270	481	17	3.4	647	28	BZ366238
409	17	3.4	574	28	BH747639	BH747639	482	17	3.4	648	10	AW552085
410	17	3.4	578	12	BU117304	BU117304	483	17	3.4	649	13	BU647740
411	17	3.4	578	12	BU117304	BU117304	484	17	3.4	649	13	BX698433
412	17	3.4	578	29	CE725339	CE725339	485	17	3.4	650	13	BQ388027
413	17	3.4	579	14	CF628962	CF628962	486	17	3.4	651	12	BM603374
414	17	3.4	580	28	AQ463929	AQ463929	487	17	3.4	651	12	BM706900
415	17	3.4	583	9	AL723998	AL723998	488	17	3.4	651	12	BM706900
416	17	3.4	583	29	CE338444	CE338444	489	17	3.4	652	13	BX483764
417	17	3.4	585	28	AZ007651	AZ007651	490	17	3.4	652	28	BZ618788
418	17	3.4	586	28	AZ108677	AZ108677	491	17	3.4	652	28	BZ618788
419	17	3.4	587	13	CB7034	CB7034	492	17	3.4	654	13	BU288602
420	17	3.4	589	9	AU020974	AU020974	493	17	3.4	655	29	CG676339
421	17	3.4	589	28	BZ148280	BZ148280	494	17	3.4	657	29	BX127461
422	17	3.4	589	28	BZ775715	BZ775715	495	17	3.4	658	28	AZ131595
423	17	3.4	590	9	AU199285	AU199285	496	17	3.4	659	9	AJ397959
424	17	3.4	591	29	CG335420	CG335420	497	17	3.4	659	28	AQ163365
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678	17	3.4	937	28	BH139313	ENTN883TR	751	16	3.2	157	29	AL771669	AL771669
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730	17	3.4	1483	11	AK035539	Mus muscu	803	16	3.2	162	16	AA011781	AA011781
731	17	3.4	1866	11	AK088565	Mus muscu	804	16	3.2	162	16	AA011781	AA011781
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this is a NIH_MGC Library."

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ORIGIN

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Db 833 GAGAGAGCCACCATTTGGC 853

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RESULT 3

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LOCUS tigr-gss-dog-17000366132442 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.

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ACCESSION CE545692
VERSION 1
KEYWORDS GSS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

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REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Kirchness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.

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TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627

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Class: shotgun.

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FEATURES

```

source
1..213
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

```

ORIGIN

```

Query Match      4.0%; Score 20; DB 29; Length 213;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 269 CCATATTGATCATCTTGGC 288
Db 190 CCATATTGATCATCTTGGC 209

```

RESULT 4

```

AQ959051/c          346 bp DNA linear GSS 28-JAN-2000
LOCUS LEREG96TR LERE Arabidopsis thaliana genomic clone LEREG96, genomic
DEFINITION

```

```

survey sequence.
ACCESSION AQ959051
VERSION AQ959051.1 GI:6786752
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 346)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TR
Class: shotgun.

```

FEATURES

```

source
1..346
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
/clone="LEREG96"
/clone_lib="LERE"
/notes="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was
sheared to 0.6-0.8 Kbp before ligation."

```

ORIGIN

```

Query Match      4.0%; Score 20; DB 28; Length 346;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 345 TTTTTCACAAAAATAACAC 364
Db 99 TTTTTCACAAAAATAACAC 80

```

RESULT 5

```

CA912211/c          360 bp mRNA linear EST 27-DEC-2002
LOCUS PCS02658 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus
DEFINITION coccineus cDNA 5' similar to Putative protein (NM_118618), mRNA
sequence.

```

```

ACCESSION CA912211
VERSION CA912211.1 GI:27399203
KEYWORDS EST.
SOURCE Phaseolus coccineus
ORGANISM Phaseolus coccineus

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.

```

```

REFERENCE 1 (bases 1 to 360)
AUTHORS Bui, A.Q., Le, B.H., Weterings, K., Bi, Y.-P., Choi, J.-S.,
McElroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and
Goldberg, R.B.

```

```

TITLE Gene Activity in Different Regions of a Post-Fertilization Plant
JOURNAL Embryo by EST Analysis
COMMENT Unpublished (2002)
Contact: Goldberg, R.B.
Department of Molecular, Cell, & Developmental Biology
University of California, Los Angeles
621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
Tel: 310 825 3270

```

Fax: 310 825 8201
Email: bobg@cla.edu
Seq primer: 5' Triplex
POLYA-No.

FEATURES

source

1. .360
/organism="Phaseolus coccineus"
/mol_type="mRNA"
/cultivar="Hammond's Dwarf Scarlet"
/db_xref="taxon:3886"
/dev_stage="6-days post-pollination"
/clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
/note="Organ: Suspensor Region of Globular-Stage Embryos;
Vector: Triplex2; Site 1: SfiIA; Site 2: SfiIB; Suspensor
regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants
[Weterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction Kit according to
the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the SfiI restriction site
of the lambda Triplex2 vector (Clontech), and the
recombinant cDNAs were transformed into E. coli XL1-Blue
cells (Clontech). Suspensor cDNA plasmids used for
directional sequencing were obtained by in vivo excision
from the lambda Triplex2 recombinants in E. coli BM25.8
cells (Clontech)."

ORIGIN

Query Match 4.0%; Score 20; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCACAAAAATAACACTTGG 368
|||||
Db 300 TCACAAAAATAACACTTGG 281

RESULT 6

BM892066/c
LOCUS 333 bp mRNA linear EST 11-MAR-2002
DEFINITION sam47h05.y1 Gm-cl069 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl069-2673 5' similar to TR:081286 O81286 T14P8.7 PROTEIN. ;,
mRNA sequence.

ACCESSION BM892066
VERSION BM892066.1 GI:19347186
KEYWORDS Glycine max (soybean)
SOURCE Glycine max

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 393)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

Putative full length read
vector to vector length is 394
Seq primer: -40RP from Gibco.

FEATURES

source

1. .393
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl069-2673"
/tissue_type="Degenerating cotyledons, 9-10 day old
etiolated seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl069"
/note="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the Bluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Query Match 4.0%; Score 20; DB 12; Length 393;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCACAAAAATAACACTTGG 368
|||||
Db 174 TCACAAAAATAACACTTGG 155

RESULT 7

AU203244

LOCUS 490 bp mRNA linear EST 17-JUL-2001

DEFINITION AU203244 unpublished oligo-capped cDNA library, stage L2

Caenorhabditis elegans cDNA clone yk818c06 5', mRNA sequence.

ACCESSION AU203244

VERSION AU203244.1 GI:14833741

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 490)

Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.

and Sugano,S.

A complementary view of the C.elegans genome

Unpublished (2001)

Contact: Yuji Kohara

Genome Biology Lab.

National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

Location/Qualifiers

1. .490

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/clone="yk818c06"

/sex="Hermaphrodite"

/tissue_type="whole animal"

/dev_stage="L2"

/clone_lib="unpublished oligo-capped cDNA library, stage

L2"

ORIGIN

Query Match 4.0%; Score 20; DB 9; Length 490;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TTTCAACAAAATAAAGCTTT 366
 |||||
 Db 443 TTTCAACAAAATAAAGCTTT 462

RESULT 8

AV960301
 LOCUS
 DEFINITION AV960301 Nori Satoh unpublished cDNA library, cleavage stage embryo
 Ciona intestinalis cDNA clone c1c12a15 5', mRNA sequence.

ACCESSION AV960301.1 GI:19448600

VERSION

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis
 Ciona intestinalis
 Ciona intestinalis
 Phlebobranchia; Chordata; Urochordata; Ascidiacea; Enterogona;

REFERENCE 1 (bases 1 to 539)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL Unpublished (2000)

COMMENT Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: sato@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source

1..539
 Location/Qualifiers
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="c1c12a15"
 /tissue_type="whole animal"
 /dev_stage="cleavage stage embryo"
 /clone_lib="Nori Satoh unpublished cDNA library, cleavage stage embryo"

ORIGIN

Query Match 4.0%; Score 20; DB 9; Length 539;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 AAGCTCTTGCTGATTTCTG 450
 |||||
 Db 211 AAGCTCTTGCTGATTTCTG 230

RESULT 9

BW204471
 LOCUS
 DEFINITION BW204471 Nori Satoh unpublished cDNA library, cleavage stage embryo Ciona
 intestinalis cDNA clone c1c1087m01 5', mRNA sequence.

ACCESSION BW204471.1 GI:24618900

VERSION

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis
 Ciona intestinalis
 Ciona intestinalis
 Phlebobranchia; Chordata; Urochordata; Ascidiacea; Enterogona;

REFERENCE 1 (bases 1 to 541)

AUTHORS Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.

TITLE Expressed genes in Ciona intestinalis (2002c)

JOURNAL Unpublished (2002)

COMMENT Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: sato@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source

1..541
 Location/Qualifiers
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="c1c1087m01"
 /tissue_type="whole body"
 /dev_stage="cleaving embryo"
 /clone_lib="Nori Satoh unpublished cDNA library, cleaving embryo"

ORIGIN

Query Match 4.0%; Score 20; DB 13; Length 541;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 AAGCTCTTGCTGATTTCTG 450
 |||||
 Db 221 AAGCTCTTGCTGATTTCTG 240

RESULT 10

LOCUS

DEFINITION

BM521341
 sal13f11.y1 Gm-c1057 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-c1057-5254 5', similar to TR:O81286 O81286 T14P8.7 PROTEIN. ;
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BM521341.1 GI:18692493
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 551)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, I., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

Seq primer: -40RP from Gibco

High quality sequence stop: 421.

FEATURES

source

1..551
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1057-5254"
 /tissue_type="Degenerating cotyledons, 2 week old seedling"
 /lab_host="DH10B"
 /clone_lib="Gm-c1057"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 4.0%; Score 20; DB 12; Length 551;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCAACAAAATAACACTTGG 368

Db 367 TCAACAAAATAACACTTGG 348

RESULT 11

BI944599/c

LOCUS

DEFINITION BI944599 557 bp mRNA linear EST 28-NOV-2001
sac44f12.y1 Gm-cl062 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl062-2952 5' similar to TR:081286 O81286 T14P8.7 PROTEIN.

;, mRNA sequence.

BI944599

BI944599.1 GI:16281655

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 557)

Shoemaker, R., Keim, P., Vodkin, L., Epelding, J., Coryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com

Seq primer: -40RP from Gibco

High quality sequence stop: 382.

Location/Qualifiers

1..557

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl062-2952"

/tissue_type="stem tissue of greenhouse grown plants"

/dev_stage="1 month old"

/lab_host="DH10B"

/clone_lib="Gm-cl062"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; The cDNA library was constructed from mRNA isolated

from stem tissue of 1 month old greenhouse grown plants

for the cultivar Raiden. Complementary DNA was

synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 4.0%; Score 20; DB 12; Length 557;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCAACAAAATAACACTTGG 368

Db 304 TCAACAAAATAACACTTGG 285

RESULT 12

BW277800

LOCUS

DEFINITION BW277800 Nori Satoh unpublished cDNA library, gastrula and neurula
Ciona intestinalis cDNA clone cign007c03 5', mRNA sequence.

ACCESSION BW277800.1 GI:24858411

VERSION

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 570)

Satou, Y., Shin, I.T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished (2002)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..570

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="cign007c03"

/tissue_type="whole body"

/dev_stage="gastrula and neurula"

/clone_lib="Nori Satoh unpublished cDNA library, gastrula

and neurula"

ORIGIN

Query Match 4.0%; Score 20; DB 13; Length 570;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 AAGCTCTTGCTGATTTCTG 450

Db 249 AAGCTCTTGCTGATTTCTG 268

RESULT 13

BQ296476/c

LOCUS

DEFINITION BQ296476

Gm-cl052-7225 5' similar to TR:081286 O81286 T14P8.7 PROTEIN. ;,

mRNA sequence.

BQ296476

VERSION

KEYWORDS

SOURCE

Glycine max (soybean)

BQ296476 574 bp mRNA linear EST 16-MAY-2002

san32g01.y2 Gm-cl052 Glycine max cDNA clone SOYBEAN CLONE ID:

Gm-cl052-7225 5' similar to TR:081286 O81286 T14P8.7 PROTEIN. ;,

mRNA sequence.

BQ296476

VERSION

KEYWORDS

SOURCE

Glycine max (soybean)

```

ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 574)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
1..574
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl052-7225"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
/clone_lib="Gm-cl052"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 1
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). The library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
University."

ORIGIN
Query Match      4.0%; Score 20; DB 13; Length 574;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 TCACAAAAATAACACTTGG 368
|||||
Db 164 TCACAAAAATAACACTTGG 145

RESULT 14
BI943495/c
LOCUS
DEFINITION
sp95c04.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl045-1375 5' similar to TR:081286 O81286 T14P9.7 PROTEIN. ;
mRNA sequence.
ACCESSION
BI943495
VERSION
BI943495.1 GI:16279552
KEYWORDS
EST.

ORGANISM      Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 577)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
Location/Qualifiers
1..577
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-1375"
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl045"
/notes="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from etiolated hypocotyl tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) primer with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by digestion with EcoRI and XhoI. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(Gibco BRL). This library was constructed by Dr. Randy
Shoemaker."

ORIGIN
Query Match      4.0%; Score 20; DB 12; Length 577;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 TCACAAAAATAACACTTGG 368
|||||
Db 333 TCACAAAAATAACACTTGG 314

RESULT 15
AZ493804
LOCUS
DEFINITION
1M0328K07R Mouse 10kb plasmid UGCGM library Mus musculus genomic
Clone UGCG1M0328K07 R, genomic survey sequence.
ACCESSION
AZ493804
VERSION
AZ493804.1 GI:10667826
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)

```

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: K column: 07
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 581.

FEATURES
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1..581
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0328K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 4.0%; Score 20; DB 28; Length 581;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 434 CTCTTGCTGATTTCTGAGC 453
Db 379 CTCTTGCTGATTTCTGAGC 398

Search completed: August 4, 2004, 15:51:10
Job time : 2464 secs